

From: Snedden, Sheridan  
Sent: Monday, February 03, 2003 7:29 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence Search 09701463

Sheridan SNEDDEN ID# 79298 Date: 2/3 /2002  
AU 1653  
308-4843  
Serial # : 09701463  
Room Location: 10A12  
Mail Box: 9B01

1). Search for SEQ ID NO: 1

Please **DO NOT SEARCH** the PENDING PATENTS Database.

Thanks,  
Examiner Snedden  
#79298  
A.U. 1653/ 9B01  
Office Location: 10A12  
Phone #: 305-4843

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 2/4/03  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: / \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

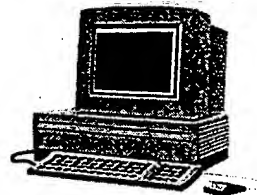
VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
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# BioTech-Chem Library

## Search Results

### Feedback Form (Optional)



Scientific & Technical Information C

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4:  
CM-1 Room 1E01

---

#### *Voluntary Results Feedback Form*

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

*Types of relevant prior art found:*

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

**Other Comments:**

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Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or [mary.hale@uspto.gov](mailto:mary.hale@uspto.gov)

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GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: February 4, 2003, 10:02:20 ; Search time 37 seconds  
(without alignments)  
993.978 Million cell updates/sec

Title: US-09-701-463-1

Perfect score: 1504  
Sequence: 1 OENODGRYSITYTGLSKH.....SCHVHSSLAQPLVFWPEAS 276

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

A.Geneseq\_101002:.\*  
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
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20: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1504	100.0	276	21	AA49442
2	910	60.5	170	21	AA43862
3	800.5	53.2	163	21	AA80275
4	791	52.6	171	20	AAV0773
5	525	34.9	274	9	AA80911
6	511	34.0	365	21	AA68268
7	511	34.0	365	21	AA52922
8	511	34.0	365	22	AA58683
9	510	33.9	93	22	AB39399
10	510	33.9	93	22	AB24181

11	510	33.9	93	22	AA60079	Human brain expres
12	510	33.9	93	22	AA72688	Human bone marrow
13	510	33.9	93	22	AA32919	Peptide #6956 enco
14	510	33.9	93	22	AB642512	Human peptide enco
15	509	33.8	369	22	AA02882	Novel human secret
16	507	33.7	365	21	AAV8266	Human leukocyte an
17	507	33.7	365	21	AAV8290	Human leukocyte an
18	507	33.7	365	21	AAV52920	HLA-A2/A28 family
19	507	33.7	365	21	AAV52924	HLA-A2/A28 family
20	507	33.7	365	22	AA58681	HLA-A2/A28 protein
21	507	33.7	365	22	AA58685	HLA-A2/A28 protein
22	505	33.6	365	21	AAV8269	Human leukocyte an
23	505	33.6	365	21	AAV52923	HLA-A2/A28 family
24	505	33.6	365	22	AA58684	HLA-A2/A28 protein
25	504	33.5	365	21	AAV8272	Human leukocyte an
26	504	33.5	365	21	AAV52926	HLA-A2/A28 family
27	504	33.5	365	22	AA58687	HLA-A2/A28 protein
28	503	33.4	274	21	AAV8276	Human leukocyte an
29	503	33.4	274	21	AAV52930	HLA-A2/A28 family
30	503	33.4	274	22	AA58691	HLA-A2/A28 protein
31	503	33.4	362	8	AAV70155	Sequence encoded b
32	503	33.4	365	21	AAV8255	Human leukocyte an
33	503	33.4	365	21	AAV8271	Human leukocyte an
34	503	33.4	365	21	AAV52919	HLA-A2/A28 family
35	503	33.4	365	21	AAV52925	HLA-A2/A28 family
36	503	33.4	365	22	AA58680	HLA-A2/A28 protein
37	503	33.4	365	22	AA58686	HLA-A2/A28 protein
38	502.5	33.4	337	8	AAV70590	Sequence of the hu
39	502	33.4	366	20	AAV07033	Breast cancer asso
40	500	33.2	274	21	AAV8275	Human leukocyte an
41	500	33.2	274	21	AAV52929	HLA-A2/A28 family
42	500	33.2	274	22	AA58690	HLA-A2/A28 protein
43	497	33.0	274	21	AAV8274	Human leukocyte an
44	497	33.0	274	21	AAV52928	HLA-A2/A28 family
45	497	33.0	274	22	AA58689	HLA-A2/A28 protein

## ALIGNMENTS

RESULT 1	AAV49442	standard; protein; 276 AA.
XX	AAV49442;	
AC	AAV49442;	
XX		
DT	17-MAR-2000	(first entry)
XX		
DE	Human plasma Zn-alpha2-glycoprotein.	
XX		
KW	Lipid mobilizing agent; zinc alpha2-glycoprotein; adenylate cyclase;	
KW	fat metabolism; muscle synthesis; obesity; type II diabetes; body weight;	
KW	muscle development; cachexia-inducing tumor; lipolysis; antitumor; cancer; human.	
XX		
OS	Homo sapiens.	
XX		
PN	W09962939-A2.	
XX		
PD	09-DEC-1999.	
XX		
PF	01-JUN-1999;	99W0-GB01509.
XX		
PR	29-MAY-1998;	98GB-0011465.
XX		
PA	(TISD/) TISDALE M J.	
PA	(TODOROV/) TODOROV P T.	
XX		
PI	Tisdale MJ, Todorov PT;	
XX		
DR	WPI; 2000-072831/06.	
XX		
PT	New lipid mobilizing agent used for treating obesity, and as diagnostic	

PT marker for cancer  
XX  
PS Claim 3: Fig 1: 63pp: English.  
XX  
CC The invention provides a therapeutic lipid mobilizing agent (I) that has  
CC the properties and characteristics of a zinc alpha2-glycoprotein, or its  
CC fragments, and had apparent relative molecular weight (Mr) determined by  
CC gel exclusion chromatography) over 6 kD. (I) stimulates adenylate cyclase  
CC activity in a guanosine diphosphate-dependent process (in murine  
CC adipocyte plasma membranes). In vivo it increases metabolism of fat and  
CC may stimulate protein (muscle) synthesis. (I) is used: to treat obesity  
CC (particularly in subjects at high risk of developing type II diabetes) or  
CC to reduce body weight; to stimulate muscle development; as diagnostic  
CC marker for cachexia-inducing tumors; to identify or investigate agents  
CC that inhibit lipolysis (potential anticachectic or anti tumor agents) and  
CC to raise specific antibodies (Ab). The Ab are used: for diagnostic  
CC detection of (I); as inhibitor or antagonist for treatment of cachexia-  
CC inducing cancers and/or tumors, and for affinity purification of (I);  
CC (I) induces a loss in body weight by specific deletion of fat; i.e. It  
CC does not reduce muscle mass. The present sequence represents the complete  
CC amino acid sequence of the human plasma Zn-alpha2-glycoprotein, as  
CC published by T. Araki et al. (1988).  
XX  
SQ Sequence 276 AA:  
Query Match 100.0%; Score 1504; DB 21; Length 276;  
Best Local Similarity 100.0%; Pred. No. 2.6e-123;  
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QENOGGRSLTYITTYGLSKHVEDVPAFOALSLNDQFRYNSKDKRSQPMGLMROVBSM 60  
DB 1 QENOGGRSLTYITTYGLSKHVEDVPAFOALSLNDQFRYNSKDKRSQPMGLMROVBSM 60  
OY 61 EDWKEDSLOKAREDMETLKDIVEYNDNSGSHVLQGRFCIEIENRRSSGAFWKYYDGG 120  
DB 61 EDWKEDSLOKAREDMETLKDIVEYNDNSGSHVLQGRFCIEIENRRSSGAFWKYYDGG 120  
OY 121 DYEENKEIPAVPDPDPAQITKQKEAPVYVQRAKAYLEECPCATLTKRYTKYSNIID 180  
DB 121 DYEENKEIPAVPDPDPAQITKQKEAPVYVQRAKAYLEECPCATLTKRYTKYSNIID 180  
OY 181 RODPSVVTSHQAPGEKKKLCIAYDPFGKIDVHMTAGOVQEPBELGDVLIHNGNGTY 240  
DB 181 RODPSVVTSHQAPGEKKKLCIAYDPFGKIDVHMTAGOVQEPBELGDVLIHNGNGTY 240  
OY 241 QSMVVVAVPDPTAPYSCVQHSLSAQLPVPWEAS 276  
DB 241 QSMVVVAVPDPTAPYSCVQHSLSAQLPVPWEAS 276  
RESULT 2  
AAB43862  
ID AAB43862 standard; Protein: 170 AA.  
XX  
AC AAB43862;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human cancer associated protein sequence SEQ ID NO:1307.  
XX  
KM Human; cancer associated gene; cancer antigen; detection; cancer;  
KM diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;  
KM antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;  
KM antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
KM dermatological; neuroprotective; thrombolytic; coagulant; neotropic;  
KM vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
KM immune disorder; haematopoietic cell disorder; autoimmune disorder;  
KM allergic reaction; graft versus host disease; organ rejection;  
KM haemostatic; thrombolytic; cardiovascular disorder; infection;  
XX  
OS Homo sapiens.  
XX

PN WO20005350-A1.  
XX  
PD 21-SEP-2000.  
XX  
PE 08-MAR-2000; 2000WO-US05882.  
XX  
PR 12-MAR-1999; 99US-0124270.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI: 2000-587533/55.  
DR N-PSDB: AAC78071.  
XX  
PT Novel isolated nucleic acids comprising sequences encoding peptides  
XX useful for treating or diagnosing e.g. cancer  
PS Claim 11; Page 1954; 2352pp; English.  
XX  
CC AAC77607 to AAC78448 encode the human cancer associated proteins given  
CC in AAB43398 to AAB44239. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vulnerable; immunomodulator;  
CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;  
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC the present invention may be used to treat immune disorders by activating  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
CC the present invention.  
XX  
SQ Sequence 170 AA:  
Query Match 60.5%; Score 910; DB 21; Length 170;  
Best Local Similarity 99.4%; Pred. No. 1.1e-71;  
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 112 FWKYYVDGKDYIEFNKEIPAVPDPDPAQITKQKEAPVYVQRAKAYLEECPCATLTKRY 171  
DB 6 FWKYYVDGKDYIEFNKEIPAVPDPDPAQITKQKEAPVYVQRAKAYLEECPCATLTKRY 65  
OY 172 LKYSNIIDRODPPSVVTSHQAPGEKKKLCIAYDPFGKIDVHMTAGOVQEPBELRGD 231  
DB 66 LKYSNIIDRODPPSVVTSHQAPGEKKKLCIAYDPFGKIDVHMTAGOVQEPBELRGD 125  
OY 232 VLIHNGNGTYQSMVVVAVPDPTAPYSCVQHSLSAQLPVPWEAS 276  
DB 126 VLIHNGNGTYQSMVVVAVPDPTAPYSCVQHSLSAQLPVPWEAS 170  
RESULT 3  
AAB80275  
ID AAB80275 standard; Protein: 183 AA.  
XX  
AC AAB80275;  
XX  
DT 24-APR-2001 (first entry)  
XX  
DE Human prostate cancer antigen #3.  
XX  
KM Immunosuppressive; neotropic; neuroprotective; antiviral; vulnerable;  
KM anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant;



CC schizophrentia, osteoporosis, arthritis, psoriasis, digestive/endocrine  
CC disorders, infections and AIDS. The human secreted proteins of the  
CC- invention are represented in AAY07744-Y07850 and the encoding nucleic  
CC acids are represented in AAX37369-X37441.

XX Sequence 171 AA:

Query Match 52.6%; Score 791; DB 20; Length 171;  
Best Local Similarity 97.3%; Pred. No. 2.9e-61;  
Matches 146; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 QENOGGRSLTITTYGLSKHVEDVPAPFQALGSLNDLQFFRRYNSKDRKSQPMGLMROVEGM 60  
DB 18 QENOGGRSLTITTYGLSKHVEDVPAPFQALGSLNDLQFFRRYNSKDRKSQPMGLMROVEGM 77  
OY 61 EDWKEDSOLQKARED--METLKDIYEYVNDNSNGSHVLOGFCFCETENNSSGAFWKYYTD 118  
DB 78 EDWKEDSOLQKAREDIEMETLKDIYEYVNDNSNGSHVLOGFCFCETENNSSGAFWKYYTD 137  
OY 119 GKDYIEFNKEIPAWVPFDPAAQITKQKWEA 148  
DB 138 GKDYIEFNKEIPAWVPFDPAAQITKQKWEA 167

RESULT 5

AAP80911  
ID AAP80911 standard; protein; 274 AA.

XX AAP80911;

DT- 18-SEP-1990 (first entry)

DE Consensus sequence of peptides which constitute the alpha-1, alpha-2 and  
alpha-3 regions of a class I HLA molecule.

DE HLA-A2 epitopes; extracellular domains alpha-1, alpha-2 and alpha-3.

XX Homo sapiens.

OS Location/Qualifiers

FT Region 1..90

FT /note="alpha-1 region"

FT Region 91..180

FT /note="alpha-2 region"

FT Region 181..272

FT /note="alpha-3 region"

XX W08805784-A.

PD 11-AUG-1988.

PF 27-FEB-1988; 88WO-US00245.

PR 30-JAN-1987; 87US-0008846.

PA (STRD ) LELAND STANFORD JR UNIV.

PI Krensky AM, Parham P, Clayberger C;

DR WPI: 1988-235147/33.

PT New peptide corresp. to major histocompatibility antigen regions -

PT transplants or auto-immune diseases

PS Example 9; Fig 4; 60pp; English.

XX The consensus sequence is derived from a total of 23 HLA-A,B,C sequences.

CC The protein sequences in the three extracellular domains (alpha-1,

CC alpha-2 and alpha-3) are shown. The example concerned the effect of

CC peptides from different HLA-A2 epitopes on cytotoxic T-lymphocyte cells by

XX CTL of different specificities.

SQ Sequence 274 AA:

Query Match 34.9%; Score 525; DB 9; Length 274;  
Best Local Similarity 39.8%; Pred. No. 9.6e-38;  
Matches 111; Conservative 47; Mismatches 105; Indels 16; Gaps 8;

OY 6 GRYSLTITTYGLSKHVEDVPAPFQALGSLNDLQFFRRYNS--KDRKSQPMGLMROVEGM 63  
DB 1 GSHSMRYFTYSVRGRGEPRIAGVYDDQFVFHFDSDAASPRMEPRAPRIELEGPEY 60  
OY 64 KEDSOLQKARED--REDMETLKDIYEYVNDNSN-GSHVLOGFCFCET--ENNSSGAFWKYY 116  
DB 61 DREIYVAQSQTDREDLRTLRG---YNNQSEAGSHITQRYACDVGSDGLNGHYA 117  
OY 117 YDKGDIYFNKEIPAWVPFDPAAQITKQKWEAPYVYQARAYLEECPATLRKYLYSK 176  
DB 118 YDKGDIYALNEDLRGWTADTAQAQITQKQWEAARV-ABQLRAYLEGTCVEMLRYLENGK 176  
OY 177 NILDRQDPSPVYVYSHQAPGEKKIKCLAYDFYPKIDVHTFRAG--QVQPEPLRGDYLH 234  
DB 177 ETLQRADEPPTKHTVTHHPISDHEATLRCAALGFYPAEITLTWQROGEDQTDTEL-VE 235  
OY 235 NNGGTYSQMWVYAVPPODTAPYSCHVQSSLAQPLVPM 273  
DB 236 AGDGTFOKMAVYVPSGEGDRTCHVQHEGLPKPLTLNW 274

RESULT 6

AAY68268  
ID AAY68268 standard; Peptide; 365 AA.

XX AAY68268;

DT 13-APR-2000 (first entry)

DE Human leukocyte antigen A2/A28 family protein SEQ ID NO:100.

XX

KM MHC class I; major histocompatibility complex; microglobulin; antigen;

KM Immune response; Immunisation; AIDS; multiple sclerosis; toxic shock;

KM cancer; lupus erythematosus; snake bite; cytostatic; antiviral;

KM immunomodulatory; dermatological; immunosuppressive; antiinflammatory;

XX

OS Homo sapiens.

PN US6011146-A.

PD 04-JAN-2000.

PF 07-JUN-1995; 95US-0481985.

PR 15-NOV-1991; 91US-0792473.

PR 05-DEC-1991; 91US-0801818.

PA (INSP ) INST PASTEUR.

PA (INRM ) INST NAT SANTE & RECH MEDICALE.

PI Kourilsky P, Moltz E, Abastado J;

DR WPI: 2000-125951/11.

PT New recombinant DNA encoding covalently linked form of major

PT histocompatibility complex Class I determinant, used for immune system

PT stimulation, e.g. for treating cancer -

PS Disclosure: Column 113-116; 88pp; English.

XX The present invention describes a recombinant DNA molecule (I)

CC containing a sequence (Ia) that encodes an altered MHC (major

CC histocompatibility complex ) Class I determinant (II) comprises a

CC polypeptide with alpha1, alpha2, alpha3 and beta2-microglobulin

CC domains, in which alpha3 and beta2 are covalently linked, thorough C-

and N-termini respectively, via a nucleotide spacer sequence encoding a



CC polypeptide. (II) includes an antigen-binding site and when (II) and  
CC the antigen are associated they are recognized by a mammalian T cell  
CC receptor (TCR). (I) are used to produce (II) which are used to study  
CC functional interactions between the various MHC domains. They can also  
CC be used to modulate (in vivo or in vitro) the immune system by inducing  
CC an effector response (cytotoxicity, antibody synthesis, phagocytosis)  
CC of immune system cells, typically for treating, or immunising against;  
CC cancer, acquired immune deficiency syndrome, lupus erythematosus,  
CC multiple sclerosis, toxic shock and snake bite, but also for selective  
CC destruction of autoreactive cells, diagnostically to assay T cell  
CC receptors and to raise specific antibodies (useful for diagnosis,  
CC therapy, studying MHC-associated cellular processes and for affinity  
CC purification). AA257558 and AA68186 to AA68316 are sequences used in  
CC the exemplification of the present invention.

SO Sequence 365 AA;

Query Match 34.0%; Score 511; DB 21; Length 365;  
Best Local Similarity 39.0%; Pred. No. 2.4e-36;  
Matches 110; Conservative 45; Mismatches 111; Indels 16; Gaps 8;

QY 6 GRYSILYITGLSKHVEDVPAFOALGSLNDQFFRYNS--KDRKSQPMGLMROYEGMEDW 63  
DB 25 GSHSMKRYFTYSVRGPEPRFIAVGVDYDFVRFSDAASQRMPEPAPWIEDEGPEYTW 84  
QY 64 KEDSOLQK-----REDMETLKDIYEYNDNSN-GSHVLYQGRGCEI-ENNRSSGAFWKY 116  
DB 85 DGETRKVKASQTHRVLDSTLRG---YYNSEASHYVQRMFGCDVSGDGFGLNGHYA 141  
QY 117 YDGDYIEFNKEIPAMVFPDPAQITKQWEAEFVYVQRAKAYLEECPPATLRKYLKYSK 176  
DB 142 YDGDYIALKEDLSWTAADMAAQTTHKWEAAHV-AEQLRAYLEGTCVEMRLRLKENGK 200  
QY 177 NILDRDPPSVVYVTSQAARGKKLCLAYDFYPGKIDVHWTRAG--QVQPEELRGDVLH 234  
DB 201 ETLQRTDAPKTHMTHNAVSDHEATLRCAWLSFYPAEITLTWQROGEQDTOTEL-VETRP 259  
QY 235 NGNGTYGSWVVAVPQDTPAYSCHVOHSSLAQPLVVPWEAS 276  
DB 260 AGDGTFOKMAVVVPSGQEQRYTCHVQHEGLPKPLTLPEWPS 301

RESULT 7  
AA52922

ID AA52922 standard; Peptide; 365 AA.

XX AA52922;

XX 14-FEB-2000 (first entry)

XX HLA-A2/A28 family peptide A2 (Lee) SEQ ID NO:100.

XX Major histocompatibility complex; MHC class I; MHC class II; antigen;  
XX Immune response; diagnosis; antibody; immunisation; autoimmune disease;  
XX acquired immune deficiency syndrome; AIDS; cytostatic; dermatological;  
XX anti-inflammatory; neuroprotective; immunosuppressive; antithyroid;  
XX vaccine; lupus erythematosus; multiple sclerosis; thyroiditis;  
XX toxic shock; tumour; snakebite.

XX Mammalia.

XX US5976551-A.

XX 02-NOV-1999.

XX 07-JUN-1995; 95US-0484905.

XX 05-DEC-1991; 91US-0801818.

XX 15-NOV-1991; 91US-0792473.

XX (INSP ) INST PASTEUR.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PI Kourilsky P, Mottez E, Abastado J;  
XX WPI; 2000-037081/03.

XX Composition containing an antigen and altered major histocompatibility  
XX Class II determinant, used to immunize against autoimmune diseases,  
XX e.g. acquired immune deficiency syndrome

PS Disclosure; Column 137-140; 96pp; English.

CC The present invention describes a composition capable of eliciting  
CC anti-major histocompatibility (MHC) antibodies. The composition  
CC comprises an antigen associated with an altered MHC Class II determinant  
CC (I) comprising alpha1, alpha2, beta1 and beta2 polypeptide domains  
CC encoded by a mammalian MHC Class II locus covalently linked to form a  
CC polypeptide (I) containing beta2, alpha2, alpha1 and beta1 domains in  
CC sequence. The resulting Antigen-MHC complex is recognizable by the T cell  
CC receptor. The compositions are used for immunisation against, or  
CC treatment of, a wide range of autoimmune diseases, e.g. acquired immune  
CC deficiency syndrome (AIDS), lupus erythematosus, multiple sclerosis,  
CC thyroiditis, toxic shock, tumour and snakebite, depending on the nature  
CC of antigen. (I) is also used to analyse functional interactions between  
CC the various domains and for targeting lymphocyte receptors. Antibodies  
CC against (I) are produced by usual methods of immunisation or cell fusion,  
CC and may be humanised by standard methods. These antibodies are useful for  
CC diagnosis (detection or purification of MHC gene products), therapy  
CC (neutralising MHC on cell surfaces) and in the study of MHC and cellular  
CC processes. AA233240 to AA233242 and AA152840 to AA152970 represent  
CC sequences used in the exemplification of the present invention.

SO Sequence 365 AA;

Query Match 34.0%; Score 511; DB 21; Length 365;  
Best Local Similarity 39.0%; Pred. No. 2.4e-36;  
Matches 110; Conservative 45; Mismatches 111; Indels 16; Gaps 8;

QY 6 GRYSILYITGLSKHVEDVPAFOALGSLNDQFFRYNS--KDRKSQPMGLMROYEGMEDW 63  
DB 25 GSHSMKRYFTYSVRGPEPRFIAVGVDYDFVRFSDAASQRMPEPAPWIEDEGPEYTW 84  
QY 64 KEDSOLQK-----REDMETLKDIYEYNDNSN-GSHVLYQGRGCEI-ENNRSSGAFWKY 116  
DB 85 DGETRKVKASQTHRVLDSTLRG---YYNSEASHYVQRMFGCDVSGDGFGLNGHYA 141  
QY 117 YDGDYIEFNKEIPAMVFPDPAQITKQWEAEFVYVQRAKAYLEECPPATLRKYLKYSK 176  
DB 142 YDGDYIALKEDLSWTAADMAAQTTHKWEAAHV-AEQLRAYLEGTCVEMRLRLKENGK 200  
QY 177 NILDRDPPSVVYVTSQAARGKKLCLAYDFYPGKIDVHWTRAG--QVQPEELRGDVLH 234  
DB 201 ETLQRTDAPKTHMTHNAVSDHEATLRCAWLSFYPAEITLTWQROGEQDTOTEL-VETRP 259  
QY 235 NGNGTYGSWVVAVPQDTPAYSCHVOHSSLAQPLVVPWEAS 276  
DB 260 AGDGTFOKMAVVVPSGQEQRYTCHVQHEGLPKPLTLPEWPS 301

RESULT 8  
AAB58683

ID AAB58683 standard; protein; 365 AA.

XX AAB58683;

XX 13-MAR-2001 (first entry)

XX HLA-A2/A28 protein #4.

XX Major histocompatibility complex; MHC class I; immune; snake bite;  
XX T cell mediated autoimmune disease; AIDS; lupus erythematosus;  
XX toxic shock.  
XX Unidentified.

PN US6153408-A.  
XX  
PD 28-NOV-2000.  
XX  
PF 09-JAN-1995; 95US-0370476.  
XX  
PR 15-NOV-1991; 91US-0792473.  
PR 07-SEP-1993; 93US-0117575.  
PR 05-DEC-1991; 91US-0801818.  
PR 07-JUN-1993; 93US-0072787.  
XX  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INST NAT SANTE & RECH MEDICAL.  
XX  
PI Abastado J, Kourilsky P, Casrouge A, Ojcius D, Lone Y, Mottez E;  
XX  
DR WPI: 2001-060089/07.  
XX  
XX  
XX New altered major histocompatibility complex (MHC) class I determinant  
PT useful for eliciting an immune response and/or for immunizing against  
PT or treating diseases, for example, multiple sclerosis, AIDS, toxic  
PT shock or snake bite .  
XX  
XX  
XX Disclosure; Column 29-33; 105pp; English.  
XX  
XX  
XX The present invention relates to a major histocompatibility complex  
CC (MHC) class I determinant, which has alpha\_1 alpha\_2 alpha\_3 and  
CC beta2-microglobulin polypeptide domains encoded by a mammalian MHC  
CC class I locus. The MHC class I determinants are useful for activating  
CC the immune system and presenting antigens to the immune system to  
CC elicit an antigenic response. The MHC class I determinants are also  
CC useful for treating diseases, e.g. T cell mediated autoimmune disease,  
CC AIDS, lupus erythematosus, toxic shock or snake bite. The altered MHC  
CC class I determinants and compositions containing antigens bound to  
CC the determinants are useful in diagnostic applications, e.g. altered  
CC determinants may be used to target lymphocyte receptors and the  
CC resulting bound determinant can be assayed.  
XX  
XX  
SQ Sequence 365 AA;

Query Match 34.0%; Score 511; DB 22; Length 365;  
Best Local Similarity 39.0%; Pred. No. 2.4e-36;  
Matches 110; Conservative 45; Mismatches 11; Indels 16; Gaps 8;  
QY 6 GSYSLIYTGSGKVEDVPAFALGSLNDLQFFRYNS--KDRKSGPMGLMROVEGMDW 63  
DB 25 GSHSRRIYFTTSVRGRGPRRIANGVDDQFVRDSDAASGRBPRAPWIEQGEPEYX 84  
QY 64 KEDSOLQKA----REDMETLKDIYEYVNDN-GSHVLDGRGCEL-ENNBSGAFWKY 116  
DB 85 DGETRKVKAKHSQTHVDLSTLRG--YYNQSEAGSHTVRMFGCDVSGDRELRGHQYA 141  
QY 117 YGKUYIENKELIPAMVPRPRAAOITKOKWEAEVYVQAKAYLEBECPATLRKYLYSK 176  
DB 142 YDGKDYIALKEIDLRSWTAADMAAQTTKKHKEAANV-AEOLRAYLEGTCEWLRKYLENK 200  
QY 177 NILDRQDPPEVVVTSHQAPGEEKKILKCLAYDFYPKIDVHWTRAG--QVQEPRLRGDVLH 234  
DB 201 ETLQRTDAKMTHTNHAASDHEATLRCWALSFPYAEITLTWQDGBDQODEL-VETRP 259  
QY 235 NGNGTYQSQVVAVVPRQDTAPYSCHVQHSLSLAQPLVWPWEAS 276  
DB 260 ASDGTGFKMAAVVPSGDEORYTCHVQHGLRPLRLPWEPS 301

RESULT 9  
ABB39399  
ID ABB39399 standard; Peptide; 93 AA.  
XX  
XX ABB39399;  
AC  
XX  
XX 04-FEB-2002 (first entry)  
DT  
XX

DE Peptide #6905 encoded by human foetal liver single exon probe.  
XX  
XX  
XX Human; foetal liver; gene expression; single exon nucleic acid probe.  
XX  
XX Homo sapiens.  
XX  
XX W0200157277-A2.  
XX  
XX  
XX 09-AUG-2001.  
XX  
XX  
XX 30-JAN-2001; 2001WO-US00669.  
XX  
XX  
XX 04-FEB-2000; 2000US-0180312.  
XX 26-MAY-2000; 2000US-0207456.  
XX 30-JUN-2000; 2000US-0608408.  
XX 03-AUG-2000; 2000US-0632366.  
XX 21-SEP-2000; 2000US-0234687.  
XX 27-SEP-2000; 2000US-0236359.  
XX 04-OCT-2000; 2000GB-0024263.  
XX  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI: 2001-483447/52.  
XX  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human fetal liver .  
XX  
XX  
XX Claim 27; SEQ ID NO 32034; 639pp + sequence listing; English.  
XX  
XX  
XX The invention relates to a single exon nucleic acid probe for  
CC measuring human gene expression in a sample derived from human foetal  
CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC fetal liver. The present sequence is a peptide encoded by a single exon  
CC nucleic acid probe of the invention.  
CC  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX  
SQ Sequence 93 AA;

Query Match 33.9%; Score 510; DB 22; Length 93;  
Best Local Similarity 98.9%; Pred. No. 4.7e-37;  
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 184 PSVVVTSHQAPGEEKKILKCLAYDFYPKIDVHWTRAGVQEPRLRGDVLHNGNGTYQSM 243  
DB 1 PSVVVTSHQAPGEEKKILKCLAYDFYPKIDVHWTRAGVQEPRLRGDVLHNGNGTYQSM 60  
QY 244 VVAVVPRQDTAPYSCHVQHSLSLAQPLVWPWEAS 276  
DB 61 VVAVVPRQDTAPYSCHVQHSLSLAQPLVWPWEAS 93

RESULT 10  
ABB24181  
ID ABB24181 standard; Protein; 93 AA.  
XX  
XX ABB24181;  
XX  
XX 23-JAN-2002 (first entry)  
XX  
XX  
XX Protein #6180 encoded by probe for measuring heart cell gene expression.  
XX  
XX  
XX Human; gene expression; heart; microarray; vascular system;  
XX cardiovascular disease; hypertension; cardiac arrhythmia;  
XX congenital heart disease.  
XX  
XX Homo sapiens.  
XX  
XX W0200157274-A2.

```

XX 09-AUG-2001.
PD
XX
PE 30-JAN-2001; 2001MO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 15; SEQ ID NO 25951; 530bp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 93 AA;
XX
Query Match 33.9%; Score 510; DB 22; Length 93;
Best Local Similarity 98.9%; Pred. No. 4.7e-37;
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 184 PPSVVTSHQAPGEEKKIKCLAYDFYFGKIDVHMTFRAGQVQPELRGVDVHNGNGTQSW 243
DB 1 PPSVVTSHQAPGEEKKIKCLAYDFYFGKIDVHMTFRAGEVQPELRGVDVHNGNGTQSW 60
XX
QY 244 VVAVPPQDTAPYSCVQHSSLAQPLVVPWEAS 276
DB 61 VVAVPPQDTAPYSCVQHSSLAQPLVVPWEAS 93
XX
RESULT 11
AAM60079
ID AAM60079 standard; Protein; 93 AA.
XX
AC AAM60079;
XX
XX 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32184.
XX
XX Human: brain expressed exon; gene expression analysis; probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX epilepsy; cancer.
XX
OS Homo sapiens.
XX
PN MO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001MO-US00667.

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XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains -
XX
PS Example 4; SEQ ID NO: 32184; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention.
XX
SQ Sequence 93 AA;
XX
Query Match 33.9%; Score 510; DB 22; Length 93;
Best Local Similarity 98.9%; Pred. No. 4.7e-37;
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
QY 184 PPSVVTSHQAPGEEKKIKCLAYDFYFGKIDVHMTFRAGQVQPELRGVDVHNGNGTQSW 243
DB 1 PPSVVTSHQAPGEEKKIKCLAYDFYFGKIDVHMTFRAGEVQPELRGVDVHNGNGTQSW 60
XX
QY 244 VVAVPPQDTAPYSCVQHSSLAQPLVVPWEAS 276
DB 61 VVAVPPQDTAPYSCVQHSSLAQPLVVPWEAS 93
XX
RESULT 12
AAM72688
ID AAM72688 standard; Protein; 93 AA.
XX
AC AAM72688;
XX
XX 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32994.
XX
XX Human: bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN MO200157276-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001MO-US00668.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.

```

XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI WPI; 2001-488900/53.  
XX  
DR  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human bone marrow -  
PS Example 4; SEQ ID NO: 32994; 658bp + Sequence Listing; English.  
XX  
PS The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukemia and myeloma. The present sequence is a  
CC protein encoded by one of the probes of the invention.  
XX  
SO Sequence 93 AA:  
Query Match 33.9%; Score 510; DB 22; Length 93;  
Best Local Similarity 98.9%; Pred. No. 4.7e-37;  
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 184 PPSVVTSHQAPGEEKKIKCLAYDFPKIDVHMTFRAGOVQPELRGDLVHNGNGTQSW 243  
Db 1 PPSVVTSHQAPGEEKKIKCLAYDFPKIDVHMTFRAGEVQPELRGDLVHNGNGTQSW 60  
QY 244 VVAVVPDPTAPYSCVHSSLAQPLVVPWEAS 276  
Db 61 VVAVVPDPTAPYSCVHSSLAQPLVVPWEAS 93  
RESULT 13  
AAM32919  
ID AAM32919 standard; Protein; 93 AA.  
XX  
AC AAM32919;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Peptide #6956 encoded by probe for measuring placental gene expression.  
XX  
KW Probe: microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200157272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000663.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-48897/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human placenta -  
XX  
PS Claim 27; SEQ ID No 33188; 654bp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes (SEN:

CC see AAI33315-AI57546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders.  
XX  
SO Sequence 93 AA:  
Query Match 33.9%; Score 510; DB 22; Length 93;  
Best Local Similarity 98.9%; Pred. No. 4.7e-37;  
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 184 PPSVVTSHQAPGEEKKIKCLAYDFPKIDVHMTFRAGOVQPELRGDLVHNGNGTQSW 243  
Db 1 PPSVVTSHQAPGEEKKIKCLAYDFPKIDVHMTFRAGEVQPELRGDLVHNGNGTQSW 60  
QY 244 VVAVVPDPTAPYSCVHSSLAQPLVVPWEAS 276  
Db 61 VVAVVPDPTAPYSCVHSSLAQPLVVPWEAS 93  
RESULT 14  
ABG42512  
ID ABG42512 standard; Peptide; 93 AA.  
XX  
AC ABG42512;  
XX  
DT 19-AUG-2002 (first entry)  
XX  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 32177.  
XX  
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW Chronic obstructive pulmonary disease; Interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tubercous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemoideriosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200186003-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000665.  
XX  
PR 04-FEB-2000; 2000US-180312P.  
PR 26-MAY-2000; 2000US-207456P.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-234687P.  
PR 27-SEP-2000; 2000US-236359P.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2002-114183/15.  
XX  
PT Spatially-addressable set of single exon nucleic acid probes, used to  
PT measure gene expression in human lung samples -  
XX  
PS Claim 27; SEQ ID No 32177; 634bp; English.  
XX  
CC The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human lung comprising single exon nucleic acid probes having one of  
CC 12614 nucleic acid sequences mentioned in the specification, or their  
CC complements or the 12387 open reading frames derived from the 12614



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OM protein - protein search, using sw model

Run on: February 4, 2003, 10:04:00 ; Search time 15 Seconds  
(without alignments)  
541.382 Million cell updates/sec

Title: US-09-701-463-1

Perfect score: 1504  
Sequence: 1 GEMQDGRYSLTYYTGLSKH.....SCHVGHSSLAQPLVPMWAS 276

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PT05\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	34.9	274	1	US-08-222-851-1
2	511	34.0	365	2	US-08-484-905-100
3	511	34.0	365	3	US-08-481-985B-100
4	511	34.0	365	4	US-08-370-476-100
5	507	33.7	365	2	US-08-484-905-98
6	507	33.7	365	2	US-08-484-905-102
7	507	33.7	365	3	US-08-481-985B-98
8	507	33.7	365	3	US-08-481-985B-102
9	507	33.7	365	4	US-08-370-476-98
10	507	33.7	365	4	US-08-370-476-102
11	505	33.6	365	2	US-08-484-905-101
12	505	33.6	365	3	US-08-481-985B-101
13	505	33.6	365	4	US-08-370-476-101
14	504	33.5	365	2	US-08-484-905-104
15	504	33.5	365	3	US-08-481-985B-104
16	504	33.5	365	4	US-08-370-476-104
17	503	33.4	365	2	US-08-484-905-108
18	503	33.4	365	3	US-08-481-985B-108
19	503	33.4	365	4	US-08-370-476-108
20	503	33.4	365	2	US-08-484-905-97
21	503	33.4	365	3	US-08-484-905-103
22	503	33.4	365	4	US-08-481-985B-97
23	503	33.4	365	3	US-08-481-985B-103
24	503	33.4	365	4	US-08-370-476-97
25	503	33.4	365	4	US-08-370-476-103
26	500	33.2	274	3	US-08-484-905-107
27	500	33.2	274	2	US-08-481-985B-107

28	500	33.2	274	4	US-08-370-476-107	Sequence 107, App
29	497	33.0	274	2	US-08-484-905-106	Sequence 106, App
30	497	33.0	274	3	US-08-481-985B-106	Sequence 106, App
31	497	33.0	274	4	US-08-370-476-106	Sequence 106, App
32	497	33.0	365	3	US-08-652-265-23	Sequence 23, App1
33	497	33.0	365	4	US-08-834-497A-23	Sequence 23, App1
34	497	33.0	365	4	US-09-503-444A-23	Sequence 23, App1
35	492	32.7	341	3	US-08-890-719-38	Sequence 38, App1
36	492	32.7	365	2	US-08-484-905-99	Sequence 99, App1
37	492	32.7	365	3	US-08-481-985B-99	Sequence 99, App1
38	492	32.7	365	4	US-08-370-476-99	Sequence 99, App1
39	491	32.6	348	3	US-08-652-265-6	Sequence 6, App1
40	491	32.6	348	4	US-08-834-497A-6	Sequence 6, App1
41	491	32.6	348	4	US-09-503-444A-6	Sequence 6, App1
42	490	32.6	274	2	US-08-484-905-105	Sequence 105, App
43	490	32.6	274	3	US-08-481-985B-105	Sequence 105, App
44	490	32.6	274	4	US-08-370-476-105	Sequence 105, App
45	490	32.6	348	3	US-08-652-265-2	Sequence 2, App1

ALIGNMENTS

RESULT 1  
US-08-222-851-1  
Sequence 1, Application US/08222851  
Patent No. 5723128  
GENERAL INFORMATION:  
APPLICANT: CLAYBERGER, CAROL A.  
APPLICANT: KRENSKY, ALAN M.  
APPLICANT: PARHAM, PETER  
TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")  
TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,851  
FILING DATE: 05-Apr-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: MILLMAN, ROBERT A.  
REGISTRATION NUMBER: 36,217  
REFERENCE/DOCKET NUMBER: 28600-20200.22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 494-0792  
TELEX: 90-4030 MRSNFOERSM  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 274 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-222-851-1  
Query Match 34.9%; Score 525; DB 1; Length 274;  
Best Local Similarity 39.8%; Pred. No. 1e-41;  
Matches 111; Conservative 47; Mismatches 105; Indels 16; Gaps 8;  
OY 6 GRYSLTYITGLSKHVEDVPAFQALGSLNDLQFRYNS--KDRKSQPMGLMRQVGEHMDW 63  
DB 1 GSHSMRYFTYSVSRPGEGEPFIAVGVDDTQFVRFSDAASPRMBRPAWIEQGEPEYW 60

QY 64 KEDSOLAKA-----REDMETLKDIYEYNDN-GSHVLOGFGCEI-ENNRSSGAFWKY 116  
Db 61 DRETOYKASQGTREDLRLTRG---YNNOSGASHTIQIMYGCDDVPDGRLLRGHYQA 117  
QY 117 YDGDYIEFNKEIPAWPFPDPAOITKQWEAPRYVQRAKALLEEBCPATLRKYLKYSK 176  
Db 118 YDGDYIALKEKLSWTADMAAOTTKKWEAAHV-ABQLRAYLEGTCEVWLKRYLNGK 176  
QY 177 NILDRDPPSVVYTSHOAPGEKKKLCLAYDPYDKIDVHWTBAG--QVQPELBDVYL 234  
Db 177 ETLORADPRPTHYTHHISHEATLRKCMALGFPAETITLWQDGEDOTDTL-VETRP 235  
QY 235 NGNGTOSWVVAVPDPTAPISCHVQSSIAQPLVWEMS 273  
Db 236 AGDGTFOKMAAVVPSGEORYTCHVQHEGLPKPLTWEPMS 274

## RESULT 2

US-08-484-905-100  
Sequence 100, Application US/08484905  
Patent No. 5976551  
GENERAL INFORMATION:  
APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: An Altered Major Histocompatibility  
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the  
NUMBER OF SEQUENCES: 127  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS-/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,905  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Potier, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 03495, 0106-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-905-100

Query Match 34.0%; Score 511; DB 2; Length 365;  
Best Local Similarity 39.0%; Pred. No. 3.2e-40;  
Matches 110; Conservative 45; Mismatches 111; Indels 16; Gaps 8;

QY 6 GRYSLTYITGSKHVEDVPAPFALGSLNDLOFFRYNS--KDRKSQPMGLRQVGMEDW 63  
Db 25 GSHSMRYFTSVSRGRGPRPIAVGVDDTQFVAFSDAASQNRPEAPAIIEDEGEPIW 84  
QY 64 KEDSOLAKA-----REDMETLKDIYEYNDN-GSHVLOGFGCEI-ENNRSSGAFWKY 116  
Db 85 DEETRKVNAHSQTHRVLDSTLNG---YNNOSGASHTIQIMYGCDDVPDGRLLRGHYQA 141  
QY 117 YDGDYIEFNKEIPAWPFPDPAOITKQWEAPRYVQRAKALLEEBCPATLRKYLKYSK 176  
Db 142 YDGDYIALKEKLSWTADMAAOTTKKWEAAHV-ABQLRAYLEGTCEVWLKRYLNGK 200  
QY 177 NILDRDPPSVVYTSHOAPGEKKKLCLAYDPYDKIDVHWTBAG--QVQPELBDVYL 234  
Db 201 ETLQRTDAPKTHMTTHAVSDHEATLRKCMALGFPAETITLWQDGEDOTDTL-VETRP 259  
QY 235 NGNGTOSWVVAVPDPTAPISCHVQSSIAQPLVWEMS 276  
Db 260 AGDGTFOKMAAVVPSGEORYTCHVQHEGLPKPLTWEPMS 301

## RESULT 3

US-08-481-985B-100  
Sequence 100, Application US/08481985B  
Patent No. 6011146  
GENERAL INFORMATION:  
APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: Altered Major Histocompatibility Complex  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,985B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495, 0106-04000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-481-985B-100

Query Match 34.0%; Score 511; DB 3; Length 365;  
Best Local Similarity 39.0%; Pred. No. 3.2e-40;









```

; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-370-476-98
```

```

Query Match 33.7%; Score 507; DB 4; Length 365;
Best Local Similarity 38.7%; Pred. No. 7.7e-40;
Matches 109; Conservative 47; Mismatches 110; Indels 16; Gaps 8;
```

```

QY 6 GRYSLTYITGLSKHVEDEVPFAQALSLNDLQFFRYNS--KDRKSQPMGLMROVEGMEDW 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 25 GSHSRHYITSLSRGRGEPRIANGYDDPQFVAFDDAASQRMPEAPWIEGGEYEW 84
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 KEDSLOKA-----REDMETLKDIVEYYNDSN-GSHVLQGRFGCEIENN-RSSGAFWKYY 116
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 85 DGEFRKVAHNSQTHRVLDSTLRG--YYNQSAGSHITQRMVGCYVSGDWFLRNGHOYA 141
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 YDKGDIYFNKEIPAWPFEDPAQITTKOKWEAEVYVORAKAYLEBECPTLRKLYLK 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 142 YDKGDIYFNKEIPAWPFEDPAQITTKOKWEAEVYVORAKAYLEBECPTLRKLYLK 200
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 NILDRQDPSPVYVNSHQAPEGKKIKLCLAYDFYPGKIDVHWTFRAG--OVQEPRLRGD 234
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 201 ETLQRTDAPKRTMTHNHAASDHEATLRCAWLSFYFAEITLTLVQRGCEQDTQDTL-VE 259
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 NGNGTQSGVVVAVVPQDTAPYSCVHQSLSLAQPLVVPWENS 276
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 260 AGDGTGFKMAVAVVPSGQEQRYTCHVQHGLPKPLLPWEP 301
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```

RESULT 10
US-08-370-476-102
; Sequence 102; Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Castongue, Armenda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-370-476-102
```

```

Query Match 33.7%; Score 507; DB 4; Length 365;
Best Local Similarity 39.3%; Pred. No. 7.7e-40;
Matches 112; Conservative 42; Mismatches 109; Indels 22; Gaps 9;
```

```

QY 6 GRYSLTYITGLSKHVEDEVPFAQALSLNDLQFFRYNS--KDRKSQPMGLMROVEGMEDW 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 25 GSHSRHYITSLSRGRGEPRIANGYDDPQFVAFDDAASQRMPEAPWIEGGEYEW 84
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 KED-----SLOKAREDMETLKDIVEYYNDSN-GSHVLQGRFGCEIENN-RSSGAFWKYY 116
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 85 DNRNRNVAQSGQTRVLDSTLRG--YYNQSAGSHITQRMVGCYVSGDWFLRNGHOYA 138
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 ---YDKGDIYFNKEIPAWPFEDPAQITTKOKWEAEVYVORAKAYLEBECPTLRKLYLK 173
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 139 QDAVDGMDYIALKEDLSRWTAADMAAQTTRKWEAAHV-AEOWRAYLEGCVEWLRRYLE 197
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 YSKNILDRQDPSPVYVNSHQAPEGKKIKLCLAYDFYPGKIDVHWTFRAG--OVQEPRLRGD 231
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 198 NKGELQRTDAPKRTMTHNHAASDHEATLRCAWLSFYFAEITLTLVQRGCEQDTQDTL-VE 256
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 VLNHNGTQSGVVVAVVPQDTAPYSCVHQSLSLAQPLVVPWENS 276
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 257 TRPADGTFKQKVAVAVVPSGQEQRYTCHVQHGLPKPLLPWEP 301
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```

RESULT 11
US-08-484-905-101
; Sequence 101; Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
```

```

1      CITY: Washington
2      STATE: D.C.
3      ZIP: 20005-3315
4
5      COMPUTER READABLE FORM:
6      MEDIUM TYPE: Floppy Disk
7      COMPUTER: IBM PC compatible
8      OPERATING SYSTEM: PC-DOS/MS-DOS
9      SOFTWARE: PatentIn Release #1.0, Version
10
11     CURRENT APPLICATION DATA:
12     APPLICATION NUMBER: US/08/484,905
13     FILING DATE: 07-JUNE-1995
14     CLASSIFICATION: 530
15
16     PRIOR APPLICATION DATA:
17     APPLICATION NUMBER: US 07/801,818
18     FILING DATE: 05-DEC-1991
19     CLASSIFICATION: 530
20
21     PRIOR APPLICATION DATA:
22     APPLICATION NUMBER: US 07/792,473
23     FILING DATE: 15-NOV-1991
24     CLASSIFICATION: 530
25
26     ATTORNEY/AGENT INFORMATION:
27     NAME: Potler, Jane E. R.
28     REGISTRATION NUMBER: 33,332
29     REFERENCE/DOCKET NUMBER: 03495.0106-03000
30
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: 202-408-4000
33     TELEFAX: 202-408-4400
34
35     INFORMATION FOR SEQ ID NO: 101:
36     SEQUENCE CHARACTERISTICS:
37     LENGTH: 365 amino acids
38     TYPE: amino acid
39     TOPOLOGY: linear
40
41     MOLECULE TYPE: peptide
42
43     US-08-484-905-101

```

Query Match	33
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Matches 110; Conservative 44; Mismatches 106; Indels

US-08-481-985B-101

Query Match	33.68; Score 505; DB 3; Length 365;
-------------	-------------------------------------

```

1  TITLE OF INVENTION:  Altered Major Histocompatibility Complex
2  TITLE OF INVENTION:
3  NUMBER OF SEQUENCES:  127
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
6  ADDRESSEE:  Dunner
7  STREET:  1300 I Street, N.W., Suite 700
8  City:  Washington
9  STATE:  D.C.
10 ZIP:  20005-3315
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE:  Floppy disk
13 COMPUTER:  IBM PC compatible
14 OPERATING SYSTEM:  PC-DOS/MS-DOS
15 SOFTWARE:  PatentIn Release #1.0, Version #1.25
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER:  US/08/370,476
18 FILING DATE:
19 CLASSIFICATION:  435
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER:  US 08/117,575
22 FILING DATE:  07-SEP-1993
23 APPLICATION NUMBER:  US 08/072,787
24 FILING DATE:  06-JUN-1993
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:  US 07/801,818
27 FILING DATE:  05-DEC-1991
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER:  US 07/792,473
30 FILING DATE:  15-NOV-1991
31 ATTORNEY/AGENT INFORMATION:
32 NAME:  Meyers, Kenneth J.
33 REGISTRATION NUMBER:  25,146
34 REFERENCE/DOCKET NUMBER:  05243.0001-01000
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE:  202-408-4000
37 TELEFAX:  202-408-4000
38 INFORMATION FOR SEQ ID NO:  101:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH:  365 amino acids
41 type:  amino acid
42 TOPOLOGY:  linear
43 MOLECULE TYPE:  peptide
44 US-08-370-476-101

```

```

Query Match          33.6%; Score 505; DB 4; Length 365;
Best Local Similarity 38.2%; Pred. No. 1,2e-39;
Matches 110; Conservative 44; Mismatches 106; Indels 28; Gaps
9;

Qy      6 GRYSLTYITYGSKNHVEDVPAFQALGSLNDLFFFRYNS--KDRKSPQMLRVQVEGMDM 63
      | :|: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      25 GSHSMKYFTYSRPGKRGEPRIAVGYVDYDQFVRRDSQAASRMRPAPWIEQSEPEY 84

Qy      64 KEDSOLQA-----REDMETLKDIVEYVYNDSN-GSHVLOGRPGCEIENNRSSCAEYK--- 114
      : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      85 DGETRKVKVKAHSQTHRDVLTSLRG---YVNSQSEAGSHLYQRMVGCY-----GFDWRFLR 135

Qy      115 ----YVYDGKDYIEFNKEIPAWVPEDPAQITKQKAEAPYVYQAKATLIEECPTLTK 170
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      136 GYHQVAVDGKDYALRKEDLRSTAAAMAQOTKHKEETAHV-AEOLRAVLEGTCEVEMLR 194

Qy      171 YLRYSKNILLDRQDPSPVAVTSHQAPBEKKKIKCLAVDFPGKIDVIMHTRAG--QVQEPET 228
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      195 YLENGEETLQRTDAPRTHMTHHAVSPDEHATLRCWALSFYPAETLLTWQRDGEQYQTDTEL 254
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      229 RGVLLNGNCTQSVWVVAVPQDTAPYSCGHVSHSLAIPLVPMWEAS 276
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      255 -VETRRDGTFFQMAVVVPSCGEORITCYHVQHEGLPKFLTPWEES 301

```

Patent No. 5976551  
GENERAL INFORMATION:  
APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: An Altered Major Histocompatibility  
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for using the  
TITLE OF INVENTION: Determinant  
NUMBER OF SEQUENCES: 127  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
ADDRESSER: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS-/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,905  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Potler, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 03495, 0106-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-905-104

Query Match	33.5%	Score 504	DB 2:	Length 365	
Best Local Similarity	39.3%	Fred. No. 1.5e-39			
Matches 112	Conservative 42	Mismatches 109	Indels 22	Gaps 9	
QY	6 GHYSLLIYITGSKIVHEDVPAFALGSLUNDLOFFRNS--KDRKSQPMGLMRQVSGMEDM	63			
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
DB	25 GSHSMKFTSTVSRRGKGEPRFIANGYDDTDFVFRPDSQAQRMHPRAPWLEQGEPEXW	84			
QY	64 -----KESDOLKAREDMETLKDIVEYNDNS-GSHVLQGRFCETIENRRSSGAEMKY-	116			
DB	85 DENTNRVAKAQSDTRDLDSTLRG---YYNQSEAGSHTIOMYMGCDV---GSDGRFLRGYR	138			
QY	117 ---YDGRDYIEFNKEIIPAWVPFPDPAQITTKQWEAEPPVYVQAQAKALEEBCATLTLLKYLK	173			
	: : :   :				
DB	139 QDAVGDQDVIALKEDRISLTAAADMAQOTTKHKEAAHV--AEQMRALLESTCEWMLRYYLE	197			
QY	174 YSKNILLDRDDPPSVVYVTSQAQFGEKKKTKLCIAYDFPGKIDVHWTFRAG--QVQEPRLRGD	231			
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
DB	198 NGKRTLTQRTDAPKTHMTHTHAVSDHEETLRCWALSFPAETLTLLWQDGDGEDQYDITDL-VE	256			
QY	232 VILHNGTQSWVVAVVPPRODTPAPYSCHHQSSLAQPLVVPWEAS	276			
	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :				
DB	257 TRDAGDGTQKWAIVVPPSGQEDQRTCHVQHEDLPRFLPLPWPPS	301			

RESULT 15  
US-08-481-985B-104  
; Sequence 104, Application US/08481985B  
; Patent No. 6011146  
ORIGINAL TRANSMISSION

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RESULT 2  
US-09-864-761-39479  
: Sequence 39479, Application US/0986476

Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecmiga-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 39479  
; LENGTH: 93  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC004977.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.4  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.94  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 16  
; OTHER INFORMATION: SWISSPROT HIT: P25311, EVALU 5.00e-53  
; US-09-864-761-39479  
Query Match 33.9%; Score 510; DB 10; Length 93;  
Best Local Similarity 98.9%; Pred. No. 4.5e-36;  
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 244 VVAVPDDTAAYSCHVQHSLSLAQPLVVPWEAS 276  
Db 61 VVAVPDDTAAYSCHVQHSLSLAQPLVVPWEAS 93  
RESULT 3  
US-10-073-300-6  
; Sequence 6, Application US/10073300  
; Publication No. US20030003535A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Yoram  
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES  
; FILE REFERENCE: 02/23339  
; CURRENT APPLICATION NUMBER: US/10/073,300  
; CURRENT FILING DATE: 2002-06-25  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 280  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-073-300-6  
Query Match 32.7%; Score 492; DB 9; Length 280;  
Best Local Similarity 37.9%; Pred. No. 5.7e-34;  
Matches 107; Conservative 48; Mismatches 111; Indels 16; Gaps 8;

QY 6 GRVSLIYITGLSKHVEYPAFOALGSLNDLOFFRYNS--KDRKSQPMGLMRQVGMEDW 63  
Db 1 GSHSMRIFFTSVSRGRGEPRIAYGVDDNQFVAFEDSDAASQMRPAPWIEQCGPEXW 60  
QY 64 KEDSOLQKA----REDMETLKDIYEYNDNS-GSHVLOGRGCEIENN-RSSGAFMKYY 116  
Db 61 DEETKRKVAHSQTHRYVDLGLTNG---YYNQSSEAGSHTVQRMGCDVGDWRFLRGYHOYA 117  
QY 117 YDGRKYIEFNKEIPAVWPDPDPAQITKOKMEAPYVVOAKAYLEECPATLRKYLYTSK 176  
Db 118 YDGRKYIEFNKEIPAVWPDPDPAQITKOKMEAPYVVOAKAYLEECPATLRKYLYTSK 176  
QY 177 NILDRDPPSVVYTSQAGGEKKLKCLAYDFYPGKIDVHWTRAG--GVQEPRLGDVYLH 234  
Db 177 ETLQRTDAPKTHMTHTHAASVDHEATLRCWALSFPYPAEITLTWQRDEDDQTDTEL-VETRP 235  
QY 235 NNGTYQSNNVAVVPRQDTAPYSCHVQHSLSLAQPLVVPWEAS 276  
Db 236 AGDGTFFQKMAVAVVPSGQEQRYTCHVQHGRLPKPLTRWEOS 277

RESULT 4  
US-10-073-300-5  
; Sequence 5, Application US/10073300  
; Publication No. US20030003535A1  
; GENERAL INFORMATION:  
; APPLICANT: Reiter, Yoram  
; TITLE OF INVENTION: SINGLE CHAIN CLASS I MAJOR HISTO- COMPATIBILITY COMPLEXES  
; FILE REFERENCE: 02/23339  
; CURRENT APPLICATION NUMBER: US/10/073,300  
; CURRENT FILING DATE: 2002-06-25  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human beta2 microglobulin linked to MHC class I heavy chain  
US-10-073-300-5

QY 184 PRSVVYTSQAGGEKKLKCLAYDFYPGKIDVHWTRAGOVQEPRLGDVYLHNGNGTYQSM 243  
Db 1 PRSVVYTSQAGGEKKLKCLAYDFYPGKIDVHWTRAGOVQEPRLGDVYLHNGNGTYQSM 60  
Query Match 32.7%; Score 492; DB 9; Length 415;  
Best Local Similarity 37.9%; Pred. No. 9.3e-34;  
Matches 107; Conservative 48; Mismatches 111; Indels 16; Gaps 8;

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Db 116 GSHSRMYFFTSVSRGCEPRFIAVGYDDIQFVFRFSDAASQRMERAPRMTQEGPEYK 175
Qy 64 KDSOLOKA-----REDMETLKDIYEYVNDNSN-GSHVLOGRFGCEIENN-KSSGAFMKYK 116
Db 176 DGETRKVAHSHQTHVNDLTGNG--YNNQSEAGSHVQRMVGCYVGDWDFLRQYHOYA 232
Qy 117 YDGDYIEFNKEIPAWVPDPAQAQITTKOKWEAEPPYVORAKAYLEEECPATLRKLYKYSK 176
Db 233 YDGDYIALKEDLSWTLAADMAAQTTKMKWEAAHV-AQOLAYLEGTCEVEMLRRLKENGK 291
Qy 177 NILDRQPPSVYVTSHQAPGKKKLCIAYDFYPKGIDVHWTFRAG--QVQEPRLGVDLH 234
Db 292 ETLRTDAPKTHMTHTHAASDHEATLRCWALSFPYPAEITLTLMQRDGEQDOTDEL-VETRP 350
Qy 235 NGNGTGYOSWVYVAVPQDTAPYSCHVOHSSLAOPLYVPMWAS 276
Db 351 AGDGTFOKMAVAVVPSGQGEORITCHVOHEGLPKPLTLRWES 392
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## RESULT 5

```
US-09-864-761-39888
Sequence 39888, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annmax Sequence Listing Engine vers. 1.1
SEQ ID NO 39888
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LENGTH: 92
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004522.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 14
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8
OTHER INFORMATION: SWISSPROT HIT: P25311, EVALUATE 9.00e-48
OTHER INFORMATION: EST_HUMAN HIT: W95318.1, EVALUATE 8.00e-47
US-09-864-761-39888
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Query Match 30.9%; Score 465; DB 10; Length 92;
Best Local Similarity 91.3%; Pred. No. 2.6e-32;
Matches 84; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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Qy 184 PPSVYVTSHQAPGKKKLCIAYDFYPKGIDVHWTFRAGQVQEPRLGVDLHNGSTYQSW 243
Db 1 PPSVYVTSHQAPGKKKLCIAYDFYPKGIDVHWTFRAGEVQEPRLGVDLHNGSTYLTW 60
Qy 244 VVAVPQDTAPYSCHVOHSSLAOPLYVPMW 275
Db 61 LVHVPQDTAPYSCHVOHSSLAOPLYVPMW 92
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## RESULT 6

```
US-09-870-521-3
Sequence 3, Application US/09870521
Patent No. US20020051989A1
GENERAL INFORMATION:
APPLICANT: Goto, Ronald
APPLICANT: Miller, Marcia
TITLE OF INVENTION: METHOD FOR BREEDING AND GENOTYPING CHICKENS AND PROBES THEREOF
FILE REFERENCE: 1954-310
CURRENT APPLICATION NUMBER: US/09/870,521
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/208471
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 332
TYPE: PRT
ORGANISM: Gallus sp.
US-09-870-521-3
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Query Match 30.5%; Score 459; DB 10; Length 332;
Best Local Similarity 37.2%; Pred. No. 4e-31;
Matches 102; Conservative 48; Mismatches 116; Indels 8; Gaps 5;
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Qy 6 GRYSTITYITGLSKHVEVPAFQALGSLNDIQFRRYNSKDKSQPMGIMRWGECHMEKE 65
Db 1 GSHSLRFLFTGMTDGPQMPRFVIVGYVDKIFGTYSKSTRAPDIYMLRQEDQENH-- 58
Qy 66 DSLOLOKAR---EDME-TLKDIYEYVNDNSNGSHVLOGRFGCEIENNRSSGAFMKYUQDGD 121
Db 59 DTOTOKAOGGERDDMINLRPERYNSKSGSHYQOMMGSCILDEGSTRGIDYAFQDGRD 118
Qy 122 YIEFNKEIPAWVPDPAQAQITTKOKWEAEPPYVORAKAYLEEECPATLRKLYKYSKNILDR 181
Db 119 FLAFDMDTMTFTAADPVAEITKRREWTEGTYAERMKHGLGTVCYONLRRLYLEHGKAALKR 178
Qy 182 QDPSPYVVTSHQAPGKKKLCIAYDFYPKGIDVHWTFRAGQVQEPRLGVDLHNGSTY 240
Db 179 RVQPEVRYWKGKADG-IITLSCHAHGFTPRITISMKDGMVRODFTRWGSIYPSDGT 237
Qy 241 QSWVYVAVPQDTAPYSCHVOHSSLAOPLYVPMW 274
Db 1 QSWVYVAVPQDTAPYSCHVOHSSLAOPLYVPMW 92
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Query Match	15.78;	Score 235.5;	DB 10;	Length 145
Best Local Similarity	38.08;	Pred. NO. 6.8e-13;		

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: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 39405
: LENGTH: 78
: TYPE: prt
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC006329.2

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; CURRENT FILING DATE: 2001-03-01
;
; PRIOR APPLICATION NUMBER: 60/186,126
;
; PRIOR FILING DATE: 2000-03-01
;
; PRIOR APPLICATION NUMBER: 60/190,479
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; PRIOR FILING DATE: 2000-05-04  
 ; PRIOR APPLICATION NUMBER: 60/206,201  
 ; PRIOR FILING DATE: 2000-05-22  
 ; PRIOR APPLICATION NUMBER: 60/218,950

; PRIOR APPLICATION NUMBER: 00/208,200  
 ; PRIOR FILING DATE: 2000-05-22  
 ; PRIOR APPLICATION NUMBER: 60/218,950  
 ; PRIOR FILING DATE: 2000-07-14



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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 4, 2003, 10:03:40 ; Search time 18 Seconds  
(Without alignments)  
1474.061 Million cell updates/sec

Title: US-09-701-463-1  
Perfect score: 1504  
Sequence: 1 OENQDGRYSLTLYTGSKH.....SCHVHSSLAQLVPEWAS 276

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1487	98.9	298	A54175	zinc-alpha-2-glyco
2	901	59.9	279	JX0353	zinc-alpha-2-glyco
3	877	58.3	290	JX0352	zinc-alpha-2-glyco
4	527	35.0	362	HLH087	MHC class I histoc
5	527	35.0	362	I59651	lymphocyte antigen
6	525	34.9	362	I37515	MHC class I histoc
7	524	34.8	362	I61865	MHC HLA-B*42, HLA-
8	522	34.7	362	S60601	HLA-B*07, HLA-
9	521	34.6	355	I80169	class I histoccompa
10	519	34.5	354	S18197	class I histoccompa
11	519	34.5	362	JH0538	class I histoccompa
12	518	34.4	354	I80165	class I histoccompa
13	518	34.4	365	I36961	MHC class I protei
14	518	34.4	365	I54493	MHC class I histoc
15	517	34.4	338	I56116	MHC HLA-B*27-HS - h
16	517	34.4	362	I68724	MHC class I histoc
17	517	34.4	365	S77963	MHC class I histoc
18	517	34.4	365	I54416	HLA-A*24 protein -
19	516	34.3	354	I80167	class I histoccompa
20	515	34.2	361	B27658	MHC class I histoc
21	515	34.2	362	HLH082	MHC class I histoc
22	514	34.2	361	I54418	MHC class I histoc
23	514	34.2	362	I72755	HLA-B*5602 - human
24	513	34.1	362	I59645	gene HLA-B protein
25	512	34.0	362	I54298	MHC class I histoc
26	511	34.0	332	S06424	MHC class I histoc
27	511	34.0	362	I68850	HLA-B*502 - human
28	510	33.9	362	I72753	HLA-B*5401 - human
29	510	33.9	362	I56130	

30	510	33.9	362	2	I81233	lymphocyte antigen
31	509	33.8	350	2	I68747	MHC class I lympho
32	509	33.8	362	2	I84431	MHC HLA-B*8 chain -
33	509	33.8	365	2	A47636	MHC class I histoc
34	509	33.8	365	2	I83063	HLA-B*5601 - human
35	508	33.8	355	2	I80171	class I histoccompa
36	508	33.8	358	2	S03538	class I histoccompa
37	508	33.8	362	2	I72754	HLA-B*5601 - human
38	508	33.8	362	2	I36962	MHC class I protei
39	508	33.8	362	2	I56133	MHC class I histoc
40	508	33.8	362	2	I54314	MHC HLA-B*39N - hum
41	508	33.8	362	2	I61904	MHC class I histoc
42	508	33.8	363	2	S03537	class I histoccompa
43	507	33.7	362	2	C35997	MHC class I histoc
44	507	33.7	362	2	I54505	lymphocyte antigen
45	507	33.7	365	2	S01171	class I histoccompa

## ALIGNMENTS

RESULT 1  
A54175  
zinc-alpha-2-glycoprotein precursor - human  
N:Alternate names: class I histocompatibility complex alpha chain homolog  
C:Species: Homo sapiens (man)  
C:Date: 13-Sep-1994 #sequence revision 18-Nov-1994 #text change 24-Nov-1999  
C:Accession: A54175; A49357; I52248; S17564; A31080; PC2210; I65208; J00946  
R:Ueyama, H.; Deng, H.X.; Ohkubo, I.  
Biochemistry 32, 12968-12976, 1993  
A:Title: Molecular cloning and chromosomal assignment of the gene for human Zn-alpha  
A:Reference number: A54175; MUID:94059971; PMID:8241150  
A:Accession: A54175  
A:Molecule type: DNA  
A:Residues: 1-298 <DEX1>  
A:Cross-references: GB:D14034; NID:9456585  
A:Note: sequence extracted from NCBI backbone (NCBI:140118, NCBI:140119)  
R:Freije, J.P.; Fueyo, A.; Uribe, J.A.; Velasco, G.; Sanchez, L.M.; Lopez-Beado, Y.S.;  
Genomics 18, 575-587, 1993  
A:Title: Human Zn-alpha-2-glycoprotein: complete genomic sequence, identification of  
A:Reference number: A49357; MUID:94140356; PMID:8307568  
A:Accession: A49357  
A:Molecule type: DNA  
A:Residues: 1-298 <FRE>  
A:Cross-references: GB:X69953; NID:9467670; PIDN:CAA49574.1; PID:9467671  
R:Ueyama, H.; Niwa, M.; Tada, T.; Sasaki, M.; Ohkubo, I.  
Biochem. Biophys. Res. Commun. 177, 656-703, 1991  
A:Title: Cloning and nucleotide sequence of a human Zn-alpha2-glycoprotein cDNA and c  
A:Reference number: I52248; MUID:91264833; PMID:2049092  
A:Accession: I52248  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 4-298 <UEY2>  
A:Cross-references: GB:D90427; NID:9220150; PIDN:BAA14417.1; PID:9220151; GB:M76707;  
A:Note: submitted to JRPD, June 1991  
R:Freije, J.P.; Fueyo, A.; Uribe, J.; Lopez-Otin, C.  
FEBS Lett. 290, 247-249, 1991  
A:Title: Human Zn-alpha(2)-glycoprotein cDNA cloning and expression analysis in benign  
A:Reference number: S17564; MUID:92008677; PMID:1915885  
A:Accession: S17564  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-298 <FUE>  
A:Cross-references: EMBL:X59766; NID:938025; PIDN:CAA42438.1; PID:938026  
R:Araki, T.; Gejyo, F.; Takagaki, K.; Haupt, H.; Schwick, H.G.; Buergli, W.; Marti, T.  
Proc. Natl. Acad. Sci. U.S.A. 85, 679-683, 1988  
A:Title: Complete amino acid sequence of human plasma Zn-alpha-2-glycoprotein and its  
A:Reference number: A31080; MUID:88124905; PMID:3422450  
A:Accession: A31080  
A:Molecule type: protein  
A:Residues: 21-84, 'E', '86-95, '98-243, 'Q', '245-298 <ARA>  
R:Takagaki, M.; Honke, K.; Tsukamoto, T.; Higashiyama, S.; Taniguchi, N.; Makita, A.;  
Biochem. Biophys. Res. Commun. 201, 1339-1347, 1994

A:Title: Zn-alpha2-glycoprotein is a novel adhesive protein.  
A:Reference number: PC2210; MUID:94296408; PMID:8024578  
A:Accession: PC2210  
A:Molecule type: protein  
A:Residues: 239-256, D, 258-265 <TRK>  
A:Experimental source: prostate, liver  
C:Genetics:  
A:Gene: GDB:AZGPI; ZAGZ  
A:Cross-references: GDB:128308; OMIM:194460  
A:Map position: 7q22.1-7q22.1  
A:Introns: 26/1 113/1 205/1  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C:Keywords: extracellular protein; glycoprotein; monomer; pyroglutamic acid; zinc  
F:1-30/boman: signal sequence #status predicted <SIG>  
F:21-298/Product: zinc-alpha-2-glycoprotein #status experimental <MAY>  
F:251-255/Region: cell attachment (R-G-D) motif  
F:251/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
F:109/Binding site: carbohydrate (Asn) (covalent) #status absent  
F:112,128,259/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:113-186, 225-280/Disulfide bonds: #status experimental

Db 2 EFGSYSLIFLYTGLSRSGKLPFRQATAPLNDQAFPHHNSNCKAAPVEPWSEIEMEDM 61  
:  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
QY KESQOLKAREd -METLKDIIVEYNDSDNGSHVLOGRPGCELENNRSSGAFMKYYIDGKD 121  
:: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db EKESQLORAREEFLVLTKDMDYEEDSTGSHFFOGFGEICETLNRRSSGAWRYAADGED 121  
  
QY 122 YIEFNKEIPAWVPDPAAQTITKOKMEAEFPYVVOAKAYLEECPATLRKLYKSKMLDR 181  
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db FIEFNKEIPAWPDPAAANTKLKMEAEKVYVQAKAYLEECPMTIKKLYISRHLD R 181  
122 FIEFNKEIPAWPDPAAANTKLKMEAEKVYVQAKAYLEECPMTIKKLYISRHLD R 181  
  
QY 182 QDPSPVAVTSQAQAGEKKLKLCLADYDFPKRIDVHWTRAQO -VOEPBELGDVLHGNGT 239  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db TDPPLVKITSVAAGGRNRIFRCCLAYDPYPQRISHHHNQASKKLASEPE -RG-VFPPNGNGT 239  
  
QY 240 YOSMWVAVVPPDTPAPYSCHVOHSLSLAQPLVWPWE 274  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db YLSMWEVEVPPQNRPFCVCHIEHKGLSQSLSVQMD 274  
  
RESULT 3  
JX0352  
zinc-alpha 2-glycoprotein - mouse  
C.Species: Mus musculus (house mouse)  
C.Date: 22-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 24-Nov-1999  
C.Accession: JX0352; I84729  
R.Ueyama, H.; Naitoh, H.; Onkubo, I.  
J. Biochem. 116, 677-681, 1994  
A.Title: Structure and expression of rat and mouse mRNAs for Zn-alpha 2-glycoprotein.  
A.Reference number: JX0352; MUID:95155283; PMID:7852290  
A.Accession: JX0352  
A.Molecule type: mRNA  
A.Residues: 1-290 <UEY>  
A.Cross-references: DDBJ:D21059  
A.Experimental source: liver  
R.Noguchi, M.; Kitabatake, A.; Ishibashi, T.; Kasahara, M.  
Immunogenetics 42, 72-74, 1995  
A>Title: The MHC class I-like Zn-alpha 2-glycoprotein gene maps to mouse chromosome 5  
A.Reference number: I49450; MUID:95317827; PMID:7792722  
A.Accession: I84729  
A.Status: preliminary; translated from GB/EMBL/DDBJ  
A.Molecule type: DNA  
A.Residues: 218-287 <RES>  
A.Cross-references: GB:I44593; NID:9995470; PID:9995471  
A.Experimental source: C57BL/6J mice  
C.Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C.Keywords: glycoprotein  
F:4-91/Region: domain A  
F:92-182/Region: domain B  
F:183-290/Region: domain C  
F:106,237/Binding site: carbohydrate (asn) (covalent) #status predicted

Db 240 YLSWAEVSPDIDPFECCLIDHGFSGSLQVMD 274

## RESULT 4

HLHUB7  
MHC class I histocompatibility antigen HLA-B7 alpha chain precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Jul-1990 #sequence\_revision 22-Apr-1995 #text\_change 01-Dec-2000  
C/Accession: B35997; A90435; A93840; I54420; I68701; A02105  
R/Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.  
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990  
A/Title: Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: frequency  
A/Reference number: A35997; MUID:90207291; PMID:2320591  
A/Accession: B35997  
A:Molecule type: mRNA  
A:Residues: 1-362 <ENR>  
A:Cross-references: GB:M32317; NID:g187786; PIDN:AAA6230.1; PID:g307221  
A/Note: this allele is designated B\*0702 (previously HLA-B\*7.2)  
R/Orr, H.T.; Lopez de Castro, J.A.; Lancet, D.; Strominger, J.L.  
Biochemistry 18, 5711-5720, 1979  
A/Title: Complete amino acid sequence of a papain-solubilized human histocompatibility  
A/Reference number: A90435; MUID:80086278; PMID:518865  
A:Accession: A90435  
A:Molecule type: protein  
A:Residues: 25-265, 'E', 267-295 <ORR>  
R/Tragardh, L.; Rask, L.; Wiman, K.; Fohlman, J.; Peterson, P.A.  
Proc. Natl. Acad. Sci. U.S.A. 77, 1129-1133, 1980  
A/Title: Complete amino acid sequence of pooled papain-solubilized HLA-A, -B, and -C anti  
A/Reference number: A93840; MUID:80145722; PMID:6928663  
A:Accession: A93840  
A:Molecule type: protein  
A:Residues: 25-42, 'Q', 44-47, 'A', 49-53, 'N', 55-68, 'Q', 70-86, 'Q', 88-93, 'H', 95-139, 'TRAI', 14  
A:Experimental source: pooled HLA-A, -B, and -C antigens  
A/Note: This sequence represents the predominant amino acid at each position  
R/Trapani, J.A.; Mickelson, C.A.; Deacon, N.J.; Hooker, D.J.; McKenzie, I.F.  
Immunogenetics 22, 399-405, 1985  
A/Title: Molecular cloning and partial nucleotide sequence of a 3.5 kb HLA-B\*27-associate  
A/Reference number: I54420; MUID:66032060; PMID:2997032  
A:Accession: I54420  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 350-362 <RES>  
A:Cross-references: GB:M15634; NID:g187661; PIDN:AAA59615.1; PID:g443670  
R/Arnott, D.; Lillie, J.W.; Auftray, C.; Kappes, D.; Strominger, J.L.  
Immunogenetics 20, 237-252, 1984  
A/Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.  
A/Reference number: I54412; MUID:84287690; PMID:6332068  
A:Accession: I68701  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 65-93, 'H', 95-362 <RE2>  
A:Cross-references: GB:M27540; NID:g187733; PIDN:AAA59638.1; PID:g386890  
C/Genetics:  
A:Gene: GDB:HLA-B  
A:Cross-references: GDB:120048; OKIM:142830  
A:Map position: 6p21.3-6p21.3  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
C/Keywords: duplication; glycoprotein; heterodimer; surface antigen; transmembrane prote  
F:1-24/Domain: signal sequence  
F:25-114/Domain: alpha-1 <EX1>  
F:115-206/Domain: alpha-2 <EX2>  
F:220-285/Domain: immunoglobulin homology <IMM>  
F:307-331/Domain: transmembrane #status predicted <TM>  
F:332-362/Domain: intracellular #status predicted <INT>  
F:110/binding site: carbohydrate (Asn) (covalent) #status experimental  
F:125-188, 227-283/Disulfide bonds: #status experimental

Query Match 35.0%; Score 527; DB 1; Length 362;  
Best Local Similarity 39.9%; Pred. No. 1,3e-32;  
Matches 113; Conservative 49; Mismatches 111; Indels 10; Gaps 7;  
OY 2 ENODGRSLTYITVGLSKHVEDVPAFOALGSLNDLQFFRYNS--KDRKSQPMGLMRQVEG 59

Db 21 ETWAGSHSMRYFYTSVSPGRGEPRFISVGYDDTQFVRFPDSDAASPREPRAPWTEDEG 80  
OY 60 MEDWKEDSLOK--AREMETLKIDVEYYNDNSN-GSHVLOGFGCEI-ENNRSSGAEFWY 115  
Db 81 PEYMDRNTQIYKAOQTRESLRNLRGYYNOSSEAGSHTLQSGCDVGPDDRLLRGHGY 140  
OY 116 YYDGKDYIEFNKEIPAWVPFPDPAQITQKWEAEVYVQRAKAYLEECPTATLRKYLKS 175  
Db 141 AYDGKDYIALMEDLRSMWTAADTAQITQKWEAAREAEOR-RAVLEGCVEMLRLRYLENG 199  
OY 176 KNIIDRODPSPVSVTSHOAPGEKKKCLAVDFYPGKIDVHWTRAG--QVQEPRLRGDYL 233  
Db 200 KDKLERADPPTVHTVTHHISDHEATLRKMGALGTFPAETLTLLWQRNGEDQDTDEL-VETR 258  
OY 234 HNGNGTQSVWVAVVPDPTAPYSCHVQSHSLAOLPLVVPWAS 276  
Db 259 PAGDRTFQKMAAVVVPSCGEORVTCVQHEGLPRPLTLRWEPSS 301

## RESULT 5

I59651  
Lymphocyte antigen - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C/Accession: I59651  
R/Amelot, K.L.; Adams, E.J.; Domene, J.D.; Parham, P.  
Tissue Antigens 44, 318-321, 1994  
A/Title: Structure of a novel subtype of B7 (B\*0705) isolated from a Chinese individu  
A/Reference number: I59651; MUID:95184211; PMID:7878658  
A:Accession: I59651  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-362 <RS>  
A:Cross-references: GB:I33922; NID:g520834; PIDN:AAA65639.1; PID:g520835  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 35.0%; Score 527; DB 2; Length 362;  
Best Local Similarity 39.9%; Pred. No. 1,3e-32;  
Matches 113; Conservative 49; Mismatches 111; Indels 10; Gaps 7;

OY 2 ENODGRSLTYITVGLSKHVEDVPAFOALGSLNDLQFFRYNS--KDRKSQPMGLMRQVEG 59  
Db 21 ETWAGSHSMRYFYTSVSPGRGEPRFISVGYDDTQFVRFPDSDAASPREPRAPWTEDEG 80  
OY 60 MEDWKEDSLOK--AREMETLKIDVEYYNDNSN-GSHVLOGFGCEI-ENNRSSGAEFWY 115  
Db 81 PEYMDRNTQIYKAOQTRESLRNLRGYYNOSSEAGSHTLQSGCDVGPDDRLLRGHGY 140  
OY 116 YYDGKDYIEFNKEIPAWVPFPDPAQITQKWEAEVYVQRAKAYLEECPTATLRKYLKS 175  
Db 141 AYDGKDYIALMEDLRSMWTAADTAQITQKWEAAREAEOR-RAVLEGCVEMLRLRYLENG 199  
OY 176 KNIIDRODPSPVSVTSHOAPGEKKKCLAVDFYPGKIDVHWTRAG--QVQEPRLRGDYL 233  
Db 200 KDKLERADPPTVHTVTHHISDHEATLRKMGALGTFPAETLTLLWQRNGEDQDTDEL-VETR 258  
OY 234 HNGNGTQSVWVAVVPDPTAPYSCHVQSHSLAOLPLVVPWAS 276  
Db 259 PAGDRTFQKMAAVVVPSCGEORVTCVQHEGLPRPLTLRWEPSS 301

## RESULT 6

I37515  
MHC class I histocompatibility antigen HLA-B\*2706 alpha chain precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jan-2000  
C/Accession: I37515  
R/Vilches, C.; de Pablo, R.; Kreisler, M.  
Immunogenetics 39, 219, 1994  
A/Title: Nucleotide sequence of HLA-B\*2706.  
A/Reference number: I37515; MUID:94102824; PMID:8276469







A;Residues: 1-338 <RES>  
 A;Cross-references: GB:M62852; NID:q187760; PIDN:AAA59647.1; PID:q187761  
 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F;196-261/Domain: immunoglobulin homology <IMM>

Query Match 34.4%; Score 517; DB 2; Length 338;

Best Local Similarity 39.1%; Pred. No. 6,7e-32;  
 Matches 109; Conservative 48; Mismatches 112; Indels 10; Gaps 7;

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QY 6 GRYSLTIYTGSLKHVEDVPAFQALGSLNDLQFFRYS--KDRKSQPMGLMRQVEGMEDW 63
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 GSHSMRYFHTSVSRPGRGEPRTITVGVDLTFVRFDSDAASPREEPRAPIEQEGPEYW 60
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 64 KEDSOL--OKAREDMETLKDIVIYYNDSN--GSHVLOGRFCCET--ENNRSQAFWKYYDG 119
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 DRETQICKAKAQTRREDLRTILRYNOSGASHLQSMGCDVGPDGRLRGHNQYAYDG 120
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 120 KDYLEFNKEIPAWVPFDPAAQITRKWEAEPPVYQAKAYLEECPPATLRKRYLKYSKNITL 179
   ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 121 KDYIALNEDLRSWTAAADTAQITQRKWEARV--AEQLRAYLEGCEVEWLRRYLENGKETL 179
   ||| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 180 DROPPPSVVVTSQAPEGKKLKLCLAYDFYPGKIDVHWTFRAG--QVQEPPELRGDVNLHNGN 237
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 180 QRADPPKTHVTHNPISDHEATLRCAWGALGFYPAEITTLTWQRDEDOQOTDEL--VETRPAGD 238
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 238 GTYQSWVYVAVVPQDTAPYSCVHOSSLAQPLVVPWEAS 276
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 239 RTFOKMAAVVPPSGEQRITCVHVEGLPKPLTLRWEPSS 277
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Search completed: February 4, 2003, 10:06:01  
 Job time : 19 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 4, 2003, 10:03:00 : Search time 11 Seconds

(without alignments)  
1040.679 Million cell updates/sec

Title: US-09-701-463-1  
Perfect score: 1504  
Sequence: 1 QENQDGRYSLTFTYITGLSKH.....SCHVHSSLAQPLVPEWEAS 276

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1487	98.9	295	1 ZA2G_HUMAN	P25311 homo sapien
2	901	59.9	296	1 ZA2G_RAT	Q63678 rattus norv
3	877	58.3	307	1 ZA2G_MOUSE	Q64726 mus musculu
4	527	35.0	362	1 IB02_HUMAN	P01889 homo sapien
5	524	34.8	362	1 IB39_HUMAN	P30460 homo sapien
6	519	34.5	362	1 IB19_HUMAN	Q08136 homo sapien
7	519	34.5	362	1 IB01_HUMAN	P30388 gorilla gor
8	518	34.4	365	1 IB01_PANTR	P16209 pan troglod
9	517	34.4	362	1 IB16_HUMAN	P30467 homo sapien
10	517	34.4	362	1 IB16_HUMAN	P19373 homo sapien
11	517	34.4	362	1 IB45_HUMAN	P30465 homo sapien
12	517	34.4	365	1 IB24_HUMAN	P05534 homo sapien
13	515	34.2	361	1 IB14_HUMAN	P03989 homo sapien
14	515	34.2	362	1 IB18_HUMAN	P10318 homo sapien
15	515	34.2	364	1 HA1B_BOVIN	P13753 bos taurus
16	514	34.2	362	1 IB59_HUMAN	P30496 homo sapien
17	513	34.1	365	1 IA23_HUMAN	P30447 homo sapien
18	512	34.0	364	1 IB24_HUMAN	P30470 homo sapien
19	512	34.0	362	1 IB22_HUMAN	P30468 homo sapien
20	511	34.0	362	1 IB15_HUMAN	P10317 homo sapien
21	511	34.0	362	1 IB32_HUMAN	P30476 homo sapien
22	510	33.9	362	1 IB27_HUMAN	P30473 homo sapien
23	510	33.9	362	1 IB55_HUMAN	P30482 homo sapien
24	510	33.9	362	1 IB57_HUMAN	P30484 homo sapien
25	509	33.8	362	1 IB04_HUMAN	P30460 homo sapien
26	509	33.8	365	1 IA11_HUMAN	P13746 homo sapien
27	508	33.8	359	1 IB01_PANTR	P16210 pan troglod
28	508	33.8	362	1 IA02_PANTR	P16210 pan troglod
29	508	33.8	362	1 IB02_PANTR	P13751 pan troglod
30	508	33.8	362	1 IB23_HUMAN	P30469 homo sapien
31	508	33.8	362	1 IB26_HUMAN	P30472 homo sapien
32	508	33.8	362	1 IB58_HUMAN	P30495 homo sapien
33	507	33.7	362	1 IB28_HUMAN	P30474 homo sapien

## ALIGNMENTS

RESULT 1	34	507	33.7	362	1	IB29_HUMAN	P18463 homo sapien
ZA2G_HUMAN	35	507	33.7	362	1	IB31_HUMAN	P30475 homo sapien
ID ZA2G_HUMAN	36	507	33.7	365	1	IA04_PANTR	P13749 pan troglod
AC P25311; 060386; STANDARD; PRT; 295 AA.	37	507	33.7	366	1	IC02_GORGO	P30388 gorilla gor
DT 01-MAY-1992 (Rel. 22, Created)	38	507	33.7	366	1	IC04_GORGO	P30387 gorilla gor
DT 01-MAY-1992 (Rel. 22, Last sequence update)	39	506	33.6	362	1	IB34_HUMAN	Q04826 homo sapien
DT 15-JUN-2002 (Rel. 41, Last annotation update)	40	505	33.6	365	1	IA03_PANTR	P13748 pan troglod
DE zinc-alpha-2-glycoprotein precursor (zn-alpha-2-glycoprotein)	41	504	33.5	362	1	IB07_HUMAN	P30462 homo sapien
DE (zn-alpha-2-GP)	42	504	33.5	362	1	IB08_HUMAN	P30463 homo sapien
GN AZGP1 OR ZAG OR ZNGP1.	43	504	33.5	362	1	IB25_HUMAN	P30471 homo sapien
OS Homo sapiens (Human).	44	504	33.5	362	1	IB35_HUMAN	P30477 homo sapien
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	45	504	33.5	362	1	IB56_HUMAN	P30493 homo sapien
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.							
OX NCBI_Taxid=9606;							
RN [1]							
RP SEQUENCE FROM N.A.							
RC TISSUE=Prostate, and Liver;							
RX MEDLINE=91264833; PubMed=2049092;							
RA Ueyama H., Niwa M., Tada T., Sasaki M., Ohkubo I.;							
RT "Cloning and nucleotide sequence of a human zn-alpha 2-glycoprotein							
RT cDNA and chromosomal assignment of its gene.";							
RL Biochem. Biophys. Res. Commun. 177:696-703(1991).							
RN [2]							
RP SEQUENCE FROM N.A.							
RC TISSUE=Mammary gland;							
RX MEDLINE=92008677; PubMed=1915885;							
RA Freije J.P., Fueyo A., Uribe J., Lopez-Otin C.;							
RT "Human Zn-alpha 2-glycoprotein cDNA cloning and expression analysis							
RT in benign and malignant breast tissues.";							
RL FEBS Lett. 290:247-249(1991).							
RN [3]							
RP SEQUENCE FROM N.A.							
RX MEDLINE=94059971; PubMed=8241150;							
RA Ueyama H., Deng H.X., Ohkubo I.;							
RT "Molecular cloning and chromosomal assignment of the gene for human							
RT zn-alpha 2-glycoprotein.";							
RL Biochemistry 32:12968-12976(1993).							
RN [4]							
RP SEQUENCE FROM N.A.							
RC TISSUE=Leukocyte;							
RX MEDLINE=94140356; PubMed=8307568;							
RA Freije J.P., Fueyo A., Uribe J.A., Velasco G., Sanchez L.M.,							
RT Lopez-Boado Y.S., Lopez-Otin C.;							
RT "Human zn-alpha 2-glycoprotein: complete genomic sequence,							
RT identification of a related pseudogene and relationship to class I							
RT major histocompatibility complex genes.";							
RL Genomics 18:575-587(1993).							
RN [5]							
RP SEQUENCE FROM N.A.							
RA Kalicki J., Harmon G.;							
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.							
RN [6]							
RP SEQUENCE OF 18-295.							
RC TISSUE=Plasma;							
RX MEDLINE=88124905; PubMed=3422450;							
RA Araki T., Gejyo F., Takagaki K., Haupt H., Schwick H.G., Buerge W.,							

RA Marti T., Schaller J., Rickli E., Brossmer R., Atkinson P.H.,  
RA Putnam F.W., Schmid K.;  
RT "Complete amino acid sequence of human plasma Zn-alpha 2-glycoprotein  
RT and its homology to histocompatibility antigens.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:679-683(1988).  
RP CHARACTERIZATION, AND CRYSTALLIZATION.  
RX MEDLINE=97272275; PubMed=9114041;  
RA Sanchez L.M., Lopez-Otin C., Bjorkman P.J.;  
RT "Biochemical characterization and crystallization of human Zn-alpha-2-  
RT glycoprotein, a soluble class I major histocompatibility complex  
RT homolog.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:4626-4630(1997).  
[6]  
RP IN VITRO BINDING OF FATTY ACID.  
RX MEDLINE=21433894; PubMed=11425849;  
RA Kennedy M.W., Heikema A.P., Cooper A., Bjorkman P.J., Sanchez L.M.;  
RT "Hydrophobic ligand binding by Zn-alpha 2-glycoprotein, a soluble  
RT fat-depleting factor related to major histocompatibility complex  
RT proteins.";  
RL J. Biol. Chem. 276:35008-35013(2001).  
[9]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
RX MEDLINE=99217440; PubMed=10206894;  
RA Sanchez L.M., Chirino A.J., Bjorkman P.J.;  
RT "Crystal structure of human ZAG, a fat-depleting factor related to MHC  
RT molecules.";  
RL Science 283:1914-1919(1999).  
CC -1- FUNCTION: Stimulates lipid degradation in adipocytes and causes  
CC the extensive fat losses associated with some advanced cancers.  
CC May bind polyunsaturated fatty acids.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Blood plasma, seminal plasma, urine, saliva,  
CC sweat, epithelial cells of various human glands, liver.  
CC -1- SIMILARITY: HIGH, TO THE EXTRACELLULAR DOMAIN OF THE ALPHA CHAIN  
CC OF CLASS I MHC ANTIGENS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC -----  
DR EMBL: D90427; BAA14417.1; -;  
DR EMBL: X59766; CAA42438.1; -;  
DR EMBL: M76707; AAB61311.1; -;  
DR EMBL: D14034; BAA03123.1; -;  
DR EMBL: X69953; CAA49574.1; ALT-INIT.  
DR EMBL: AC004522; AAC09483.1; -;  
DR PIR: A31080; A31080.  
DR PIR: J00946; J00946.  
DR PDB: 1ZAG; 31-MAR-99.  
DR SWISS-2DPAGE: P25311; HUMAN.  
DR GeneW: HGNC:910; AZGP1.  
DR MIM: 194460; -;  
DR InterPro: IPR003006; Iq\_MHC.  
DR InterPro: IPR003597; Iq\_C1.  
DR InterPro: IPR001039; MHC\_I.  
DR Pfam: PF00047; Iq\_2.  
DR Pfam: PF00129; MHC\_I\_2.  
DR ProDom: PD000050; MHC\_I\_1.  
DR SMART: SM00407; IG1; 1.  
DR PROSITE: PS00290; IG\_MHC; 1.  
KW Glycoprotein; Signal; 3D-structure.  
FT SIGNAL 1 17  
FT CHAIN 18 295  
FT MOD\_RES 18 18 ZINC-ALPHA-2-GLYCOPROTEIN.  
FT DISULFID 120 183 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 222 277  
FT CARBOHYD 109 109  
FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .).  
FT N-LINKED (GLCNAC. . .).  
FT N-LINKED (GLCNAC. . .).

FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .).  
FT CONFLICT 1 2 MV -> MWASRMAL (IN REF. 2).  
FT CONFLICT 82 82 O -> E (IN REF. 6).  
FT CONFLICT 93 94 MISSING (IN REF. 6).  
FT CONFLICT 241 241 E -> O (IN REF. 6).  
FT CONFLICT 266 295 PPTPACSTAAAPSPSCGPRARCKGLEAMDLRRSCPS  
FT CLMELNHRNHSOM IHKA (IN REF. 5).  
SQ SEQUENCE 295 AA; 33872 MW; 6C6A7541A2B6371A CRC64;  
Query Match 98.9%; Score 1487; DB 1; Length 295;  
Best Local Similarity 98.6%; Pred. No. 1.5e-107;  
Matches 274; Conservative 2; Mismatches 0; Indels 2; Gaps 1;  
QY 1 QENODGRYSLTYYTGLSKHVEDYPAFOALGSLNDLOFFRYNSKDRSOMGLMROVEGM 60  
DB 18 QENODGRYSLTYYTGLSKHVEDYPAFOALGSLNDLOFFRYNSKDRSOMGLMROVEGM 77  
QY 61 EDWKEDSOLKARDD-METLKDIYERYNDSNGSHVLOGRGCEIENNRSSGAFWKYYD 118  
DB 78 EDWKEDSOLKARDDMETLKDIYERYNDSNGSHVLOGRGCEIENNRSSGAFWKYYD 137  
QY 119 GKDYIEFNKEIPAWVPDPDPAQITKQWEAPYVORAKAYLEECATILKTYKSKI 178  
DB 138 GKDYIEFNKEIPAWVPDPDPAQITKQWEAPYVORAKAYLEECATILKTYKSKI 197  
QY 179 LDRQDPSPVVTSHQAPGEKKKLCIADYFPYKIDVHWTFAGOVPELRLGVLHNGG 238  
DB 198 LDRQDPSPVVTSHQAPGEKKKLCIADYFPYKIDVHWTFAGOVPELRLGVLHNGG 257  
QY 239 TYOSWVVAVPPDPTAPPSCHVOHSSLAOPLVPMWEAS 276  
DB 258 TYOSWVVAVPPDPTAPPSCHVOHSSLAOPLVPMWEAS 295  
RESULT 2  
ZAG\_RAT ZAG\_RAT STANDARD; PRT; 296 AA.  
AC Q63678; Q63523;  
ID 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DR 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Zinc-alpha-2-glycoprotein precursor (Zn-alpha-2-glycoprotein)  
DE (Zn-alpha-2-GP).  
CN AZGP1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=95155283; PubMed=7852290;  
RA Ueyama H., Naitoh H., Onkudo I.;  
RT "Structure and expression of rat and mouse mRNAs for Zn-alpha 2-  
RT glycoprotein.";  
RL J. Biochem. 116:677-681(1994).  
RN [2]  
RP SEQUENCE OF 4-296 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=9433816; PubMed=8056339;  
RA Fuenyo A., Uria J.A., Freije J.M.P., Lopez-Otin C.;  
RT "Cloning and expression analysis of the cDNA encoding rat Zn-alpha 2-  
RT glycoprotein.";  
RL Gene 145:245-249(1994).  
CC -1- FUNCTION: STIMULATES LIPID DEGRADATION IN ADIPOCYTES AND CAUSES  
CC THE EXTENSIVE FAT LOSSES ASSOCIATED WITH SOME ADVANCED CANCERS (BY  
CC SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BUT NOT IN A WIDE NUMBER  
CC OF TISSUES, INCLUDING PROSTATE, MAMMARY GLAND, KIDNEY, INTESTINE,  
CC LUNG, PANCREAS, OVARY, UTERUS, THYROID, PLACENTA, SPLEEN, BRAIN  
CC AND HEART.

CC -1- SIMILARITY: HIGH, TO THE EXTRACELLULAR DOMAIN OF THE ALPHA CHAIN  
CC OF CLASS I MHC ANTIGENS.  
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CC -----  
DR EMBL: D21058; BAA04637.1; -;  
DR EMBL: X75309; CAA53057.1; -;  
DR HSSP: P25311; 1ZAG.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003600; Ig\_Like.  
DR InterPro: IPR001039; MHC\_I.  
DR Pfam: PF00129; MHC\_I; 1.  
DR ProDom: PD000050; MHC\_I; 1.  
DR SMART: SM00410; Ig\_Like; 1.  
DR PROSITE: PS00290; IG\_MHC; FALSE\_NEG.  
KW Glycoprotein; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 296  
FT MOD\_RES 18 18  
FT FT  
FT FT  
FT DISULFID 118 181  
FT DISULFID 220 275  
FT CARBOHYD 123 123  
FT CARBOHYD 254 254  
FT CONFLICT 120 120  
FT CONFLICT 194 194  
SQ SEQUENCE 296 AA; 34017 MW; 1259467DD18D453A CRC64;  
Query Match 59.3%; Score 901; DB 1; Length 296;  
Best Local Similarity 60.0%; Pred. No. 1.9e-62;  
Matches 165; Conservative 39; Mismatches 65; Indels 6; Gaps 4;  
QY 4 QDGRYSLTFTYTGSLSKHVEDVPAFOALGSLNDLOFFRYNSKDRKSQPMGLMROVEGEMDW 63  
DB 19 ETGSYSTLFYLTGSLRSKGLPRFOATAFLNDQAFHYNSNGSGAEVPEVMSHGEEDW 78  
QY 64 KEDSOLAKARED--METLKDIVEYNDNSGSHVLOGFGEIENNRSSGAFWKYYIDGKD 121  
DB 79 EKESQLOARAREEFLVYLKIDIMYEDSTSGHTEFGMGCEITNNRSSGAVWRAYDGED 138  
QY 122 YIEFNKEIPAWVPDPDPAQAQITKQKWEAPYVORAKAYLEECPPATLRYLKYLSKNTLDR 181  
DB 139 FIEFNKEIPAWIPDPDPAANTATKLWEAEKYYVORAKAYLEECPTMLKYLTSRSHLDR 198  
QY 182 ODPPSVVVTSHOAPGEKKKLCIAYDFYPGKIDVHWTRAQ--VQPELGGDVLHNGNGT 239  
DB 199 TDDPYTKITSRVAPGRNRIRFRCIAYDFYPPQISLHWNQASKKLAFEE-EG-VFPNGNGT 256  
QY 240 YOSMVVAVVPDQDAPYSCVHQSLSLAQPLVPEME 274  
DB 257 YLSMVEVPEPQNRDPFVCHIEHKLGSQSLSTVQMD 291  
RESULT 3  
ZAG\_MOUSE  
ID ZAG\_MOUSE STANDARD: PRT: 307 AA.  
AC 064726;  
DT 01-NOV-1997 (rel. 35, Created)  
DT 01-NOV-1997 (rel. 35, Last sequence update)  
DT 01-NOV-1997 (rel. 35, Last annotation update)  
DE zinc-alpha-2-glycoprotein precursor (zinc-alpha-2-glycoprotein)  
DE (zinc-alpha-2-Gp).  
GN Azgp1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BAI/C; TISSUE=Liver;  
RX MEDLINE=95155283; PubMed=7852290;  
RA Ueyama H., Naitoh H., Ohkubo I.,  
RT "Structure and expression of rat and mouse mRNAs for Zn-alpha 2-  
RT glycoprotein."  
RL J. Biochem. 116:677-681(1994).  
RN [2]  
RC SEQUENCE OF 235-304 FROM N.A.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=95317827; PubMed=7797272;  
RA Noguchi M., Kitabatake A., Ishibashi T., Kasahara M.;  
RT "The MHC class I-like Zn-alpha 2-glycoprotein gene maps to mouse  
RT chromosome 5".  
RL Immunogenetics 42:72-74(1995).  
CC -1- FUNCTION: STIMULATES LIPID DEGRADATION IN ADIPOCYTES AND CAUSES  
CC THE EXTENSIVE FAT LOSSES ASSOCIATED WITH SOME ADVANCED CANCERS (BY  
CC SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: HIGH, TO THE EXTRACELLULAR DOMAIN OF THE ALPHA CHAIN  
CC OF CLASS I MHC ANTIGENS.  
CC -----  
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CC -----  
DR EMBL: D21059; BAA04638.1; -;  
DR EMBL: D44593; BAA07996.1; -;  
DR HSSP: P25311; 1ZAG.  
DR MGD: MGI:103163; Azgp1.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003600; Ig\_Like.  
DR InterPro: IPR001039; MHC\_I.  
DR Pfam: PF00129; MHC\_I; 1.  
DR ProDom: PD000050; MHC\_I; 1.  
DR SMART: SM00410; Ig\_Like; 1.  
DR PROSITE: PS00290; IG\_MHC; FALSE\_NEG.  
KW Glycoprotein; Signal.  
FT SIGNAL 1 17  
FT CHAIN 18 307  
FT MOD\_RES 18 18  
FT FT  
FT FT  
FT DISULFID 118 181  
FT DISULFID 220 275  
FT CARBOHYD 123 123  
FT CARBOHYD 190 190  
FT CARBOHYD 254 254  
SQ SEQUENCE 307 AA; 35256 MW; 4754524C76187A10 CRC64;  
Query Match 58.3%; Score 877; DB 1; Length 307;  
Best Local Similarity 59.3%; Pred. No. 1.4e-60;  
Matches 163; Conservative 36; Mismatches 70; Indels 6; Gaps 4;  
QY 4 QDGRYSLTFTYTGSLSKHVEDVPAFOALGSLNDLOFFRYNSKDRKSQPMGLMROVEGEMDW 63  
DB 19 ETGSYSTLFYLTGSLRSKGLPRFOATAFLNDQAFHYNSNGSGAEVPEVMSHGEEDW 78  
QY 64 KEDSOLAKARED--METLKDIVEYNDNSGSHVLOGFGEIENNRSSGAFWKYYIDGKD 121  
DB 79 EKESQLOARAREEFLVYLKIDIMYEDSTSGHTEFGMGCEITNNRSSGAVWRAYDGED 138  
QY 122 YIEFNKEIPAWVPDPDPAQAQITKQKWEAPYVORAKAYLEECPPATLRYLKYLSKNTLDR 181  
DB 139 FIEFNKEIPAWIPDPDPAANTATKLWEAEKYYVORAKAYLEECPTMLKYLTSRSHLDR 198  
QY 182 ODPPSVVVTSHOAPGEKKKLCIAYDFYPGKIDVHWTRAQ--VQPELGGDVLHNGNGT 239  
DB 199 TDDPYTKITSRVAPGRNRIRFRCIAYDFYPPQISLHWNKANKKLAFEE-EG-VFPNGNGT 256

OY 240 YQSWVVAVVPDTRAPVSGHVHSSLAQPLVYPWE 274  
 DB 257 YLSMAEVEYSPDIDPFPLIDHRSQSLSYQMD 291

RESULT 4  
 1B02\_HUMAN STANDARD; PRT; 362 AA.  
 ID 1B02\_HUMAN  
 AC 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE HLA class I histocompatibility antigen, B\*7 B\*0702 alpha chain precursor (B7.2).  
 GN HLA-B OR HLAB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90207291; PubMed=2320591;  
 RA Ennis P.D., Zemmour J., Salter R.D., Parham P.;  
 RT "Rapid cloning of HLA-A,B CDNA by using the polymerase chain  
 reaction: frequency and nature of errors produced in amplification.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90315860; PubMed=2700944;  
 RA Parham P., Benjamin R.J., Chen B.P., Clayberger C., Ennis P.D.,  
 RA Krensky A.M., Lawlor D.A., Littman D.R., Norment A.M., Orr H.T.,  
 RA Salter R.D., Zemmour J.;  
 RT "Diversity of class I HLA molecules: functional and evolutionary  
 interactions with T cells.";  
 RL Cold Spring Harb. Symp. Quant. Biol. 54:529-543(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85287366; PubMed=2993161;  
 RA Sood A.K., Pan J., Biro P.A., Pereira D., Srivastava R., Reddy V.B.,  
 RA Ducean B.W., Weissman S.M.;  
 RT "Structure and polymorphism of class I MHC antigen mRNA.";  
 RL Immunogenetics 22:101-121(1985).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Ellexson M.E., Zhang L., Hildebrand W.H.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 25-295.  
 RX MEDLINE=80088278; PubMed=518865;  
 RA Orr H.T., Lopez de Castro J.A., Lancel D., Strominger J.L.;  
 RT "Complete amino acid sequence of a papain-solubilized human  
 histocompatibility antigen, HLA-B\*7.2. Sequence determination and  
 search for homologues.";  
 RL Biochemistry 18:5711-5720(1979).  
 CC -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 THE IMMUNE SYSTEM.  
 CC -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 MICROGLOBULIN).  
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 CC -----  
 DR EMBL: M32317; AAA36230.1; -  
 DR EMBL: M16102; AAA59622.1; ALT\_SEQ.  
 DR EMBL: U29057; AAA91229.1; -  
 DR PIR: A02185; HLH087.  
 DR PIR: B35997; B35997.

DR HSSP: P30460; 1ACD.  
 DR Genew; HGNC:4932; HLA-B.  
 DR MIM; 142830; -  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003597; IG\_c1.  
 DR InterPro: IPR001039; MHC\_I.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGc1; 1.  
 DR ProSite; PS00290; IG\_MHC; 1.  
 KM MHC I; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362  
 FT  
 FT DOMAIN 25 114  
 FT DOMAIN 115 206  
 FT DOMAIN 207 298  
 FT DOMAIN 299 309  
 FT TRANSMEM 310 333  
 FT DOMAIN 334 362  
 FT CARBOHYD 110 110  
 FT DISULFID 125 188  
 FT DISULFID 227 283  
 FT CONFLICT 15 18 AALA -> GPW (IN REF. 3).  
 FT CONFLICT 266 266 Q -> E (IN REF. 5).  
 FT CONFLICT 268 268 R -> S (IN REF. 3).  
 FT CONFLICT 297 297 R -> G (IN REF. 3).  
 FT CONFLICT 314 315 GL -> RP (IN REF. 3).  
 SQ SEQUENCE 362 AA; 40460 MW; 5E5A7BDE031403D6 CnC64;

Query Match 35.0%; Score 527; DB 1; Length 362;  
 Best Local Similarity 39.9%; Pred. No. 1,4e-33;  
 Matches 113; Conservative 49; Mismatches 111; Indels 10; Gaps 7;

OY 2 ENODGRVSTITYTYTGSKRVEDVPAPFALGSLNDLOFPFRYNS-KDRKSQPMGLROYEG 59  
 DB 21 ETWAGSHSMRPYPTVSRSRGKEPRPISGVYDDPQFVFDSDASPREPPAPMTEQEG 80  
 OY 60 MEDWKEEDSOLQK-AREDMETLKDIIVEYNDSEN-GSHVLQGRFGEI-ENNRSSGAFWKY 115  
 DB 81 PEYWDKNTQIYKAQOTDESLRNLRGYNOSEASHLQSYNGGDYGPDRLLRGHDQY 140  
 OY 116 YYDGKDYIEFNKEIPAWPFPPAQTITKOKWEAEFYVYORAAKYLEECFATLRLKYKYS 175  
 DB 141 AYDGKDYIALNDELSMTADTAQTITKOKWEAEAEAEQR-RAYLEGCEVEWLRYLENG 199  
 OY 176 KNILDRQDPSPVYVYSHQAPGEEKLKCLAYDFYGGKIDVHMTFRAG-QVQPEELRGDVL 233  
 DB 200 KKLKERADPPKTHVYHHPISDHEATLRWALGFYPAEITLTWQROGEDQDTDTL-VEYR 258  
 OY 234 HNGNGYQSWVVAVVPDTRAPVSGHVHSSLAQPLVYPWEAS 276  
 DB 259 PAGDRTFQKMAVVPVSGEQRKTYCHVQHEGLPKPLTLFWMS 301

RESULT 5  
 1B39\_HUMAN STANDARD; PRT; 362 AA.  
 ID 1B39\_HUMAN  
 AC P30480;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE HLA class I histocompatibility antigen, BW-42 B\*4201 alpha chain precursor.  
 GN HLA-B OR HLAB.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89235215; PubMed=2715640;



Qy	116	YVDDKDVTEEFKKEIPAWPPRPAPQITKKWEAEPPVYQRAKALTEECSPATLEKRYKYS	175
Db	141	AYDKEDYALIEDLSMTAAADTAQAOTTKRKEAAR-EAEQIRALLEGECVWLRRIYENG	199
Qy	176	KNIDRDDPPPEVVVTSHPAPEKRRKCLADFFYPGKIDVMTBAG-QVQPELRDVL	233
Db	200	KETIGRADPRPTVTHHPIDSHDEATLRQMALGFPAAETITLWQDGEDQDQDTEL-VETR	258
Qy	234	HNGCTIOSVVVAVAPRODTPAPYSCHVQSHSLAOPLYVWPMAS	276
Db	259	PAGDRTFOKMAAVVVPSCGEORVYCHVQHEGLPRPLTWBPS	301
RESULT 7			
ID	10KO.GORGO	STANDARD;	PRT; 362 AA.
AC	P30388;		
DT	01-APR-1993 (Rel. 25, Created)		
DT	01-APR-1993 (Rel. 25, Last sequence update)		
DT	01-APR-1993 (Rel. 25, Last annotation update)		
DS	Class I histocompatibility antigen, GOGO-OKO alpha chain precursor.		
OS	Gorilla gorilla gorilla (Lowland gorilla).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Gorilla.		
OX	NCBI_TaxID=9595;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92078860; PubMed=1744581;		
RT	*LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;		
RT	*GORILLA CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX ALLELES: COMPARISON		
RL	TO HUMAN AND CHIMPANZEE CLASS I.*;		
RL	J. EXP. MED. 174:1491-1509(1991).		
CC	-I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO		
CC	THE IMMUNE SYSTEM.		
CC	-I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-		
CC	MICROGLOBULIN).		
CC	-----		
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CC	-----		
DR	EMBL; X60692; CAA43100.1; -		
DR	PIR; JH0538; JH0538.		
DR	HSSP; P30685; IABE.		
DR	InterPro; IPR003006; IG-MHC.		
DR	InterPro; IPR003597; IG.C1.		
DR	InterPro; IPR001039; MHC_I.		
DR	Pfam; PF00047; Ig_1.		
DR	Pfam; PF00129; MHC_I; 1.		
DR	ProDom; PD000050; MHC_I; 1.		
DR	SMART; SM00407; IG.C1.		
DR	PROSITE; PS00290; IG-MHC; 1.		
KW	MHC I; Transmembrane; Glycoprotein; Signal.		
FT	SIGNAL	1	24
FT	CHAIN	25	362
FT			
FT	DOMAIN	25	114
FT			
FT	DOMAIN	115	206
FT			
FT	DOMAIN	207	298
FT			
FT	DOMAIN	299	308
FT			
FT	TRANSMEM	309	332
FT			
FT	DOMAIN	333	362
FT			
FT	DISULFID	125	188
FT			
FT	DISULFID	227	283
FT			
FT	CAROHND	110	110
FT			
SO	SEQUENCE	362 AA;	40755 MW; BFE49DA72C55649D CRC64;
Query Match 34.5%; Score 519; DB 1; Length 362;			

Best Local Similarity 39.3%, Pred. No. 5.9e+33, Indels 22; Gaps 9;  
Matches 112; Conservative 46; Mismatches 105;

	RESULT 8		
1A01_PANTR	PANTR		
ID	1A01_PANTR	STANDARD:	PRT: 365 AA.
AC	P16209;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-APR-1990 (Rel. 14, Last sequence update)		
DT	01-APR-1993 (Rel. 25, Last annotation update)		
DE	CH1A class I histocompatibility antigen, A-2 alpha chain precursor.		
OS	Pan troglodytes (Chimpanzee).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Euheria; Primates; Catarrhini; Hominiidae; Pan.		
OX	NCBI_Taxid=9598;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90201944; PubMed=1690682;		
RA	Lawlor D.A., Warren E., Ward F.E., Parham P.;		
FT	"Comparison of class I MHC alleles in humans and apes.";		
RL	Immunol. Rev. 113:147-185(1990)."		
CC	-I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.		
CC	-I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).		
CC	-----		
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CC	-----		
DR	EMBL; M30678; AAA87970.1; -.		
DR	HSSP; Q95352; IHHR.		
DR	InterPro; IPRO03006; IG_MHC.		
DR	InterPro; IPRO03597; IG_CL.		
DR	InterPro; IPRO01039; MHC_I.		
DR	Pfam; PF00047; ig_1.		
DR	Prodrom; PD000050; MHC_I; 1.		
DR	SMART; SMO0407; IGc1_1.		
DR	PROSITE; PS00290; IG_MHC; 1.		
KM	MHC I; Transmembrane; Glycoprotein; Signal.		
FM	SIGNAL	1	24
FT	CHAIN	25	365
FT			
FT	DOMAIN	25	114
FT	DOMAIN	115	206
FT	DOMAIN	207	298
FT	DOMAIN	299	308
FT			
			CH1A CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.





```
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CC -----
DR EMBL: M54883; AAA59616.1;
DR HSSP: P03989; IHSa.
DR MIM: 142830;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00129; MHC_I; 1.
DR PRODOM: PD000050; MHC_I; 1.
DR SMART: SM00407; IgC1; 1.
DR PROSITE: PS00290; Ig_MHC; 1.
DR MHC I; Transmembrane; Glycoprotein; Signal.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 B-27 B*2703 ALPHA CHAIN.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT DOMAIN 110 110 CYTOPLASMIC TAIL.
FT CARBOHYD 125 188 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT DISULFID 227 283 BY SIMILARITY.
FT SEQUENCE 362 AA; 40402 MW; 8CC7B45FE899036 CRC64;

Query Match 34.4%; Score 517; DB 1; Length 362;
Best Local Similarity 38.5%; Pred. No. 8.5e-33;
Matches 109; Conservative 49; Mismatches 115; Indels 10; Gaps 7;

QY 2 ENODGRYSLTITYTGLSKHVEDVPAFQALGSLNDQFFRYNS-KDRKSOPMGLMROYEG 59
DB 21 ETWAGSHSMRYHTSRSRGEPRTITGYDDTLFVFDSDATSPKREPAPIEDBG 80
QY 60 MEDWKEDSOL-QKAREMETLKDIVEYYNDSN-GSHVLOGRFGEI-ENNSSGAF 115
DB 81 PEHWBRETOICKAKQOTDEDETRTLRYNOSEAGSHTLQNNYCGDVGPDGRLRGYHOD 140
QY 116 YVDGKDYIEFNKEIPAWVPDPAPAOITTKQWEAEPPYVORAKAYLEEECPATLRKLYKS 175
DB 141 AYDGKDYIALNEDLSWTADTAQAQITQKKEAARV-ABQALRAYLEGCEVEMLRRL 199
QY 176 KNILDRQDPSPVYVYSHQAPGEKKLCLAYDFYFGKIDVHMTFRAG-QVQPEELRG 233
DB 200 KETLQRADPRKQVHTHNPISDHEATLRCWALGFPYPAETILITQORCEDEDTOTEL-VETR 258
QY 234 HNGNGTYGSMVYVAVPDPDTAPYSCVHQSLSAOLPLVWMEAS 276
DB 259 PAGDRTFQKMAVAVVPSGGEORYTCHVQHEGLPKPLTLMEPS 301

RESULT 11
1B45_HUMAN
ID 1B45_HUMAN STANDARD: PRT: 362 AA.
AC P30485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, BW-47 B*4701 alpha chain
DE precursor.
GN HLA-B OR HLAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBL_TaxID=9606;
OX 11
RN SEQUENCE FROM N.A.
RP MEDLINE=8152906; PubMed=3257938;
RX Zemmour J., Enlis P.D., Parham P., Dupont B.;
RA "Comparison of the structure of HLA-Bw47 to HLA-B13 and its
RT relationship to 21-hydroxylase deficiency.";
```

```
RL Immunogenetics 27:281-287(1988).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: M19756; AAA52664.1;
DR HSSP: P03989; IHSa.
DR MIM: 142830;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00129; MHC_I; 1.
DR PRODOM: PD000050; MHC_I; 1.
DR SMART: SM00407; IgC1; 1.
DR PROSITE: PS00290; Ig_MHC; 1.
DR MHC I; Transmembrane; Glycoprotein; Signal.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362
FT DOMAIN 25 114 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 115 206 BW-47 B*4701 ALPHA CHAIN.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-1.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 309 332 EXTRACELLULAR ALPHA-3.
FT DOMAIN 333 362 CONNECTING PEPTIDE.
FT DOMAIN 110 110 CYTOPLASMIC TAIL.
FT CARBOHYD 125 188 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT DISULFID 227 283 BY SIMILARITY.
FT SEQUENCE 362 AA; 40571 MW; ED3EACB8C15EAE CRC64;

Query Match 34.4%; Score 517; DB 1; Length 362;
Best Local Similarity 39.2%; Pred. No. 8.5e-33;
Matches 112; Conservative 45; Mismatches 113; Indels 16; Gaps 8;

QY 2 ENODGRYSLTITYTGLSKHVEDVPAFQALGSLNDQFFRYNS-KDRKSOPMGLMROYEG 59
DB 21 ETWAGSHSMRYHTSRSRGEPRTITGYDDTLFVFDSDATSPKREPAPIEDBG 80
QY 60 MEDWKEDSOLQKAREMETLKDIVEYYNDSN-GSHVLOGRFGEI-ENNSSGAF 112
DB 81 PEHWBRETOICKAKQOTDEDETRTLRYNOSEAGSHTLQNNYCGDVGPDGRLRGY 137
QY 113 WKYYDGKDYIEFNKEIPAWVPDPAPAOITTKQWEAEPPYVORAKAYLEEECPATLRKYL 172
DB 138 HODAYDGKDYIALNEDLSWTADTAQAQITQKKEAARV-ABQALRAYLEGCEVEMLRRL 196
QY 173 KYSKNLDRQDPSPVYVYSHQAPGEKKLCLAYDFYFGKIDVHMTFRAG-QVQPEELRG 230
DB 197 ENGKETLQRADPRKQVHTHNPISDHEATLRCWALGFPYPAETILITQORCEDEDTOTEL-V 255
QY 231 DYLHNGNGTYGSMVYVAVPDPDTAPYSCVHQSLSAOLPLVWMEAS 276
DB 256 ETRPAGDRTFQKMAVAVVPSGGEORYTCHVQHEGLPKPLTLMEPS 301

RESULT 12
1A24_HUMAN
ID 1A24_HUMAN STANDARD: PRT: 365 AA.
AC P05534; P30448; P30449; Q95355;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE HLA class I histocompatibility antigen, A-24(A-9) alpha chain
```



```

DE precursor (AW-24) .
OS HLA-A OR HLA-B .
OC Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (A*2401) .
RX MEDLINE=65206128; PubMed=2987115;
RT N' Guyon C., Sodoyer R., Trucy J., Strachan T., Jordan B.R.;
RT "The HLA-A*24 gene: sequence, surroundings and comparison with the
RT HLA-A2 and HLA-B genes."
RN [2]
RN Immunogenetics 21:479-489(1985) .
RP REVISIONS (A*2401) .
RA Jordan B.R.;
RL Submitted (XXX-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A. (A*2402/A*2403) .
RX MEDLINE=92104637; PubMed=1729171;
RT Little A.-M., Madrigal J.A., Parham P.;
RT "Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.",
RN [4]
RN Immunogenetics 35:41-45(1992) .
RP SEQUENCE FROM N.A. (A*2402) .
RX MEDLINE=92269955; PubMed=1317015;
RT Belich M.P., Madrigal J.A., Hildebrand W.H., Zemmour J.,
RT Williams R.C., Luz R., Petzl-Erler M.L., Parham P.;
RT "Unusual HLA-B alleles in two tribes of Brazilian Indians."
RN [5]
RN Nature 357:326-329(1992) .
RP SEQUENCE FROM N.A. (A*2402) .
RX MEDLINE=98007772; PubMed=9349616;
RT Lafont M., Froelich N., Parisiadis A., Bausinger H., Pfeiffer B.,
RT Tongio M.M.;
RT "An intronic mutation responsible for a low level of expression of an
RT HLA-A*24 allele."
RN [6]
RN Tissue Antigens 50:340-346(1997) .
RP SEQUENCE OF 26-206 FROM N.A.
RA Gao X., McCluskey J.;
RA Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (A*2408) .
RT TISSUE=Blood;
RA Kashiwase K.; Tokunaga K., Ishikawa Y., Qiu L., Furuya M.,
RA Sawanaka K., Akaza T., Tadokoro K., Fujii T.;
RT "A new A9 sequence HLA-A9HH from Japanese."
RN [8]
RN MHC 3:9-14(1996) .
RP FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
RP THE IMMUNE SYSTEM.
CC -I SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) .
CC -I POLYMORPHISM: THE FOLLOWING ALLELES OF A-24 ARE KNOWN: A*2401,
CC A*2401, A*2403 AND A*2408 (A9HH). THE SEQUENCE SHOWN IS THAT OF
CC A*2401.
CC -----
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CC -----
DR EMBL, M15497; AAA59611.1; -
DR EMBL, M64740; AAA59600.1; -
DR EMBL, M64741; AAA59601.1; -
DR EMBL, U19733; AAB60651.1; -
DR EMBL, U18987; AAB60651.1; JOINED.
DR EMBL, Z72422; CAAG6532.1; -
DR EMBL, D83516; BAAL1936.1; -
DR HSSP; Q93532; IHHK.

```

[illegible]

OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. PubMed=3912316;  
 RX MEDLINE=86138405; Weis E.H., Kuon W., Doerner C., Lang M., Riethmuller G.;  
 RA "Organization, sequence and expression of the HLA-B\*27 gene: a  
 RT molecular approach to analyze HLA and disease associations";  
 RL Immunobiology 170:367-380(1985).  
 RN [2]  
 RP SEQUENCE OF 25-361 FROM N.A.  
 RX MEDLINE=86149317; PubMed=3485286;  
 RA Szeles H., Riethmuller G., Weiss E., Meo T.;  
 RT "Complete sequence of HLA-B\*27 cDNA identified through the  
 RT characterization of structural markers unique to the HLA-A, -B, and  
 RT -C allelic series";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).  
 RN [3]  
 RP SEQUENCE OF 25-295.  
 RX MEDLINE=85226361; PubMed=2408663;  
 RA Ezquerro A., Bragado R., Vega M.A., Strominger J.L., Woody J.,  
 RT Lopez de Castro J.A.;  
 RT "Primary structure of papain-solubilized human histocompatibility  
 RT antigen HLA-B\*27";  
 RL Biochemistry 24:1733-1741(1985).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.  
 RX MEDLINE=92405152; PubMed=1525820;  
 RA Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;  
 RT "The three-dimensional structure of HLA-B\*27 at 2.1 Å resolution  
 RT suggests a general mechanism for tight peptide binding to MHC";  
 RL Cell 70:1035-1048(1992).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=92018187; PubMed=1922337;  
 RA Madden D.R., Gorga J.C., Strominger J.L., Wiley D.C.;  
 RT "The structure of HLA-B\*27 reveals a nonamer self-peptides bound in an  
 RT extended conformation";  
 RL Nature 353:321-325(1991).  
 CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  
 CC THE IMMUNE SYSTEM.  
 CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN).  
 CC -I- DISEASE: THIS PROTEIN CORRELATES WITH THE DEVELOPMENT OF  
 CC ANKYLOSING SPONDYLITIS.  
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 CC -----  
 CC EMBL, X03945; CAA27578.1; ALT\_TERM.  
 DR PIR: A25128; HLHUB2.  
 DR PIR: S07441; S07441.  
 DR PDB: 1HSA; 15-OCT-92.  
 DR MIM: 142830;  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR001039; MHC\_I.  
 DR Pfam: PF00047; Ig\_1.  
 DR Pfam: PF00129; MHC\_I\_1.  
 DR ProDom: PD000050; MHC\_I\_1.  
 DR SMART: SM00407; IgC1\_1.  
 DR PROSITE: PS00290; Ig\_MHC\_1.  
 KM MHC\_I: Transmembrane; Glycoprotein; Signal; 3D-structure.  
 FT SIGNAL 1 24  
 FT CHAIN 25 361 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,  
 FT B-27 ALPHA CHAIN.

FT DOMAIN 25 114  
 FT DOMAIN 115 206  
 FT DOMAIN 207 298  
 FT DOMAIN 299 308  
 FT TRANSMEM 309 332  
 FT DOMAIN 333 361  
 FT CARBOHYD 110 110  
 FT DISULFID 125 188  
 FT DISULFID 227 283  
 FT CONFLICT 206 206  
 FT CONFLICT 266 266  
 FT STRAND 27 38  
 FT TURN 39 41  
 FT STRAND 42 52  
 FT TURN 53 54  
 FT STRAND 55 61  
 FT TURN 62 63  
 FT STRAND 70 71  
 FT HELIX 74 76  
 FT TURN 77 78  
 FT HELIX 81 108  
 FT TURN 109 110  
 FT TURN 113 114  
 FT STRAND 118 127  
 FT TURN 129 130  
 FT STRAND 133 142  
 FT TURN 143 144  
 FT STRAND 145 150  
 FT TURN 152 153  
 FT STRAND 157 159  
 FT HELIX 162 173  
 FT TURN 174 175  
 FT HELIX 176 185  
 FT TURN 186 186  
 FT HELIX 187 198  
 FT TURN 199 199  
 FT HELIX 200 203  
 FT TURN 204 204  
 FT STRAND 207 207  
 FT STRAND 210 217  
 FT STRAND 222 233  
 FT STRAND 238 243  
 FT TURN 244 245  
 FT STRAND 246 247  
 FT HELIX 249 251  
 FT STRAND 253 254  
 FT STRAND 258 259  
 FT STRAND 265 274  
 FT TURN 275 276  
 FT HELIX 278 280  
 FT STRAND 281 286  
 FT TURN 288 289  
 FT STRAND 294 296  
 SQ SEQUENCE 361 AA; 40464 MW; 2F8293299B52A47F CRC64;  
 Query Match 34.2%; Score 515; DB 1; Length 361;  
 Best Local Similarity 38.5%; Pred. No. 1.2e-32;  
 Matches 109; Conservative 49; Mismatches 115; Indels 10; Gaps 7;  
 QY 2 ENODGRYSLTLYTGTGSKHEDVDPFAFGALGSLNDLQFFRYNS--KDRKSQPMGLMROYEG 59  
 DB 21 ETWAGSHSMRYFHTSVSRGREGPRFTTYGYVDLFLVAFDSDASPREPRAPMIEDOG 80  
 QY 60 MEDWEDSQL--OKAREDETAKDIVEYYNSN--GSHVLQGRFGCEI--ENRSSGAFMKY 115  
 DB 81 PEYWDRETIKAKAQTDREDLRTILRYNQSEAGSHTLQNNYGCDDVGPDRLLRGYHD 140  
 QY 116 YTDGADYIEFNKEIPAWVFPDPAQITKQKWAPEYVYQRAAYLEEDCPATLRKYKYS 175  
 DB 141 AYDGKYLINLDELDSMTADTAQAQITQKKWEAARY-ABQLRAYLEGCEVLEWLRYLENG 199  
 QY 176 KNLIDRODPESVYVYVSHQAPGKKKLKCLAYDFYDGKIDVHMTTRAG--QVDEPELRGDLV 233

[illegible]

```

DR PROSITE: PS00290; IG-MHC: 1.
KW MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 362 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 25 114 B-27 B*2705 ALPHA CHAIN.
FT FT 115 206 EXTRACELLULAR ALPHA-1.
FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.
FT DOMAIN 299 308 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 309 332 CONNECTING PEPTIDE.
FT DOMAIN 333 362 CYTOPLASMIC TAIL.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT DISULFD 125 188 BY SIMILARITY.
FT DISULFD 227 283 BY SIMILARITY.
SQ SEQUENCE 362 AA; 40428 MW; C8D2F154E3292031 CRC64;

Query Match 34.2%; Score 515; DB 1; Length 362;
Best Local Similarity 38.5%; Pred. NO. 1.2e-32;
Matches 109; Conservative 49; Mismatches 115; Indels 10; Gaps 7;

OY 2 EMODRYSLTITYYTSLKSHVEDVPAFOALGSLNDLOFPYRNS-KDRKSQPMGLMROVEG 59
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 EFWASHSHMRHYHTSVSRGREGPERFITYGYVDLTLFPRFSDASPREPRAPYIDEQG 80
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 60 MEDKEDSOL-QKAREDMEITLKDIVEXYDNS-GSHVLCGREGCI-ENNSSGAFMKY 115
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 81 PEYMDREIQICKAKQOTREDRLTLRLRYNQGSEASHFLQNNWYGCDVGDGRLLRGYHOD 140
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 116 YYDGNDYIEFNKEIPAWVPEDPAQITQKMAEYVYQAKAYILEECPALRLRYLAKS 175
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 141 AVDGKDYIALNEDLSSWPAADTAADITQKRWMAAV-AEQLRAYLEGCEVTLRLRYLNG 199
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 176 KNLIDROPSPVSVSHQAPGKKTKLCLAYFGYCKIDVHTFRAG-QVOPEPLRGDVL 233
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 200 KETLORADPRKPTHVHHNPISDEHAILRCMALGFYAEITLTITMQRGGEQYQDTEL-VETR 258
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 234 HNGNGTYQSWVAVVPDPTAFYSCYHOSSLAQPLVYVWEAS 276
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 PAGDRTPQKMAVVVPSCGEGRYTCVQHGGELPKPLTLRMERS 301
   1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
HA1B-BOVIN STANDARD: PRT; 364 AA.
AC P13753:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE BOLA class I histocompatibility antigen, alpha chain BL3-7 precursor.
OS Bos taurus (bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
DX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258075; PubMed=3133413;
RA Enlis P.D., Jackson A.P., Parham P.;
RT "Molecular cloning of bovine class I MHC cDNA.";
RL J. Immunol. 141:642-651(1988).
JC 1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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```



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OM protein - protein search, using sw model

Run on: February 4, 2003, 10:03:20 ; Search time 33 Seconds

(Without alignments)  
1723.303 Million cell updates/sec

Title: US-09-701-463-1

Perfect score: 1504  
Sequence: 1 QENQDGRVLTYYITGLSKH.....SCHVOHSLAQPLVPEWAS 276

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	871	57.9	307	11 Q9DBB7	Q9dbb7 mus musculu
2	527	35.0	336	7 Q19782	Q19782 homo sapien
3	527	35.0	362	7 Q29854	Q29854 homo sapien
4	527	35.0	362	7 Q31613	Q31613 homo sapien
5	526	35.0	362	7 Q9P9P5	Q9P9P5 homo sapien
6	526	35.0	362	7 P79489	P79489 homo sapien
7	523	34.8	356	7 Q30221	Q30221 ateles belz
8	523	34.8	362	7 Q9MXK1	Q9mxk1 pan troglod
9	523	34.8	362	7 Q29681	Q29681 homo sapien
10	523	34.8	362	7 Q9MXK4	Q9mxk4 pan troglod
11	522	34.7	357	7 Q30894	Q30894 pithecia pl
12	522	34.7	362	7 Q29638	Q29638 homo sapien
13	522	34.7	362	7 Q29861	Q29861 homo sapien
14	521	34.6	355	7 Q9MXJ8	Q9mxj8 pan troglod
15	521	34.6	355	7 Q95529	Q95529 pan troglod
16	520	34.6	357	7 Q30895	Q30895 pithecia pl

17	520	34.6	362	7 Q9MXL9	Q9mxl9 pan troglod
18	520	34.6	362	7 Q9TPW6	Q9tpw6 homo sapien
19	520	34.6	362	7 Q9MXI0	Q9mxio pan troglod
20	520	34.6	362	7 P79612	P79612 homo sapien
21	520	34.6	362	7 Q29846	Q29846 homo sapien
22	520	34.6	362	7 Q29718	Q29718 homo sapien
23	519	34.5	354	7 Q95412	Q95412 hyllobates l
24	519	34.5	354	7 Q78204	Q78204 gorilla gor
25	519	34.5	362	7 Q29705	Q29705 homo sapien
26	519	34.5	362	7 P79555	P79555 homo sapien
27	518	34.4	354	7 Q95525	Q95525 pan paniscu
28	518	34.4	365	7 Q29689	Q29689 homo sapien
29	517	34.4	298	7 Q9GJF1	Q9gjf1 homo sapien
30	517	34.4	362	7 Q9GJL3	Q9gj13 homo sapien
31	517	34.4	362	7 Q29693	Q29693 homo sapien
32	517	34.4	365	7 Q95J06	Q95j06 homo sapien
33	516	34.3	354	7 Q95527	Q95527 pan paniscu
34	516	34.3	362	7 Q9MXH0	Q9mxh0 pan troglod
35	516	34.3	362	7 Q9MYB8	Q9myb8 homo sapien
36	516	34.3	362	7 Q30720	Q30720 macaca mula
37	516	34.3	365	7 Q9XRX7	Q9xrx7 pongo pygma
38	515	34.2	360	7 Q95396	Q95396 bos taurus
39	515	34.2	362	7 Q78189	Q78189 homo sapien
40	515	34.2	365	7 Q9MY51	Q9my51 homo sapien
41	514	34.2	346	7 Q30897	Q30897 pithecia pl
42	514	34.2	357	7 Q9MXI3	Q9mx13 pan troglod
43	514	34.2	359	7 Q29934	Q29934 homo sapien
44	514	34.2	362	7 Q9MXH5	Q9mxh5 pan troglod
45	514	34.2	365	7 Q8WLD0	Q8wld0 pan troglod

## ALIGNMENTS

RESULT 1	ID	Q9DBB7	PRELIMINARY:	PRT:	307 AA.
AC	Q9DBB7				
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DE	01-JUN-2002	(TREMBLrel. 21, Last annotation update)			
DE	Alpha-2-glycoprotein 1, zinc.				
GN	AZGP1				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=LIVER;				
RX	MEDLINE=21085660; Pubmed=11217851;				
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kodota K., Matsuda H.A., Ashburner M., Batalov S., Casavani T.,				
RA	Eisenschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schirml L.M., Staabli F., Suzuki K., Tomita M., Wagner L., Washio T.,				
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Blake J., Boffelli D., Bojunga N., Carinici P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki K., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,				
RA	Hayashizaki Y.,				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
DR	EMBL; AK005051; BAB23777.1; -;				
	HSSP; P25311; 12AG.				





QY 176 KNILRODPPSVVYTSQAAPGEEKKLCLAYDFPGKIDVHNTFRAG--QVQEPRLRGDVL 233  
ID 030221 PRELIMINARY; PRT; 362 AA.  
AC P79489;  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
DE HLA-B\*5504.  
GN HLA-B\*5504.  
OS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BLLOOD;  
RA Bannai M., Tokunaga K., Tanaka H., Kashiwase K., Lin L., Tokunaga K.,  
RA Fuji T.;  
RT "Five HLA-B\*22 group alleles in Japanese."  
RL Tissue Antigens 0:0-0(1997).  
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
CC IMMUNE SYSTEM (BY SIMILARITY).  
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
CC MICROGLOBULIN) (BY SIMILARITY).  
DR EMBL; D85761; BAA12868.1; -.  
DR HSSP; P30460; IAGD.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001039; MHC\_I.  
DR Pfam; PF00047; Ig\_1.  
DR Pfam; PF00129; MHC\_I\_1.  
DR PRINTS; PR01638; MHCCLASSI.  
DR PRODOM; PD000050; MHC\_I\_1.  
DR SMART; SM00407; IgC1\_1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Glycoprotein; Transmembrane.  
SQ SEQUENCE 362 AA; 40484 MW; 2FEE2B98C0B5F5BF CRC64;

Query Match 35.0%; Score 526; DB 7; Length 362;  
Best Local Similarity 39.6%; Pred. No. 2,4e-37;  
Matches 112; Conservative 48; Mismatches 113; Indels 10; Gaps 7;

QY 2 ENQDGRYSITLYITGSLKSHVEDVPAFQALGSLNDIQFFRYNS--KDRKSQPMGLMROVEG 59  
DB 21 EFWASHSKRYTYTAMSRGRGEPRIAVGYDDTQFVFFDSDAASPREPRAPMTEQSG 80  
QY 60 MEDMKEDSLOLK--AREDMETLKDIYEYNDN--GSHVLQGRFGCEI--ENNSSGAFMW 115  
DB 81 PEYWRNTOIYKAQOTDRESLRNLRGYNSQSEAGSHLQSMYGCQVGPDRGLLRHNGY 140  
QY 116 YDGDYIEFNKEIPAWPEPDPAQITKQKMEAPRYVORAKAYLEECRPALRLKYLKS 175  
DB 141 AYDGDYIALNEDLSRMTAADPAADITQKRWBAARV--AQQLRAYLEGTCVEMLRILENG 199  
QY 176 KNILRODPPSVVYTSQAAPGEEKKLCLAYDFPGKIDVHNTFRAG--QVQEPRLRGDVL 233  
DB 200 KETLQADPPKTHVTHHPISDHEATLRCAWALGFYPAEITLITQRODGEDTOTDEL-VEFR 258  
QY 234 HNGNGTYQSQSVVAVVAPPODTAPYSCHVQSSSLAOPLVVWEMS 276  
DB 259 PAGDRPFQKMAVAVVPSGGEORVYTCVQHEGLPKPLTLRWEMS 301

RESULT 7  
Q030221 PRELIMINARY; PRT; 356 AA.  
ID 030221  
AC Q030221;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
DE MHC class I Atbe-B\*01 (Fragment).  
GN ARBE-B.  
OS Ateles belzebuth (Long-haired spider monkey).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.  
OX NCBI\_TaxID=9507;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98070787; PubMed=9405648;  
RA Cadavid L.F., Shuffelbotham C., Ruiz F.J., Yeager M., Hughes A.L.,  
RA Watkins D.I.;  
RT "Evolutionary instability of the major histocompatibility complex  
RT class I loci in new world primates."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:14536-14541(1997).  
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
CC IMMUNE SYSTEM (BY SIMILARITY).  
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
CC MICROGLOBULIN) (BY SIMILARITY).  
DR EMBL; U59648; AB97491.1; -.  
DR HSSP; O19673; IHSB.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR001039; MHC\_I.  
DR Pfam; PF00047; Ig\_1.  
DR Pfam; PF00129; MHC\_I\_1.  
DR PRINTS; PR01638; MHCCLASSI.  
DR PRODOM; PD000050; MHC\_I\_1.  
DR SMART; SM00407; IgC1\_1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Glycoprotein; Transmembrane.  
FT NON\_TER 1  
SQ SEQUENCE 356 AA; 39667 MW; 9011AB221B79191B CRC64;

Query Match 34.8%; Score 523; DB 7; Length 356;  
Best Local Similarity 39.1%; Pred. No. 4,2e-37;  
Matches 113; Conservative 50; Mismatches 104; Indels 22; Gaps 9;

QY 2 ENQDGRYSITLYITGSLKSHVEDVPAFQALGSLNDIQFFRYNSKDR--KSQPMGLMROVEG 59  
DB 13 OTRASHSMRYTYTSVRGRGEPRIAVGYDDTQFVFFDSDAIIPMEPRALMMEQEG 72  
QY 60 MEDMKEDSLOLKA-----REDMETLKDIYEYNDN--GSHVLQGRFGCEIENNSSGAFW 113  
DB 73 PEYWEQTRRVAQAOTDVRDLQTLRG--YNSQSEAGSHLQTMIGCDV--GEGRFL 126  
QY 114 KYE----YDGDYIEFNKEIPAWPEPDPAQITKQKMEAPRYVORAKAYLEECRPALRL 169  
DB 127 RGYRQADAYGKRYIALNEDLSRMTAADMAAONTKRWMEANV--AQQLRAYLEGKQOESLR 185  
QY 170 KYLYSKNILRODPPSVVYTSQAAPGEEKKLCLAYDFPGKIDVHNTFRAG--QVQEP 227  
DB 186 RYLENGKETLQADPPKTHVTHHPVSDHEATLRCAWALGFYPREITLITQRODGEDTOTDE 245  
QY 228 LRGDVLHNGNGTYQSQSVVAVVAPPODTAPYSCHVQSSSLAOPLVVWEMS 276  
DB 246 L-VEFRPAGDRTFQKMAVAVVPSGGEORVYTCVQHEGLPEPLTLRWEMS 293  
RESULT 8  
ID Q9MXK1 PRELIMINARY; PRT; 362 AA.  
AC Q9MXK1;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
DE MHC class I antigen.



GN PATR-B.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
 RX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=20322475; PubMed=10866106;  
 RA de Groot N.G., Olling N., Arguello R., Watkins D.I., Doxiadis G.G.M.,  
 RA Madrigal J.A., Bontrop R.E.;  
 RT "Major histocompatibility complex class I diversity in a West African  
 chimpanzee population: implications for HIV research.";  
 RL Immunogenetics 51:398-409(2000).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
 CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN) (BY SIMILARITY).  
 DR EMBL; AF168410; AAF72791.1; -.  
 DR HSSP; P03989; IJSA.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PRO1638; MHCCLASSI.  
 DR PRODOM; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; Igcl; 1.  
 DR PROSITE; PS00290; Ig\_MHC; 1.  
 KW Glycoprotein; Transmembrane.  
 SQ SEQUENCE 362 AA; 40442 MW; 4E1A081945D3A4F3 CRC64;

Query Match 34.8%; Score 523; DB 7; Length 362;  
 Best local similarity 39.6%; Pred. No. 4.3e-37;  
 Matches 112; Conservative 46; Mismatches 115; Indels 10; Gaps 7;

QY 2 ENODGRSLTYITVGLSKHVEDPAPFQALGSLNDLOEFRRYSKDR--KSOQPMGLMROVEG 59  
 Db 21 ETWAGSQSMRYFTYSVRSGRGPREFISGVYDDTQFVRFSDDAASPREBRRAWIEDEG 80  
 QY 60 MEDKEDSO--LQKAREMETLKDIIVEYNDN--GSHVLQGRFGEI--ENNRSSGAFWKY 115  
 Db 81 PEYMDRNTQITKTNTQDRESLRNLRGYNDSEAGSHTLQSMYGGDMDPDRLLRGHDY 140  
 QY 116 YDDKDYIEFKETIPAWPFPDPAOITKQKWEAEPPVYVQRAKAYLEECPTLTKRYLYKS 175  
 Db 141 AYDGDYIALNWDLSRWADTAOITQKWEARENR--RAYLEGCVEMLRYLENG 199  
 QY 176 KNILRDPPPSVVVTSHQAPGEKKLKCLAYDFYPGKIDVHWTRAG--QVOEPELRGDVL 233  
 Db 200 KETIQRADPRKTHVTHHPSIDEHATLRQWALGFYPAETITLWQDGEEDQTDTEL-VETR 258  
 QY 234 HNGKTYOSWVVAVPPDPTAPYCHVQHSSLAQPLVVPWEAS 276  
 Db 259 PAGDRTFQKMAVVVPSGEQRYTCHVQHEGLPKPLTLRWEPS 301  
 RESULT 9  
 Q29681 PRELIMINARY; PRT; 362 AA.  
 ID Q29681;  
 AC Q29681;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE MHC class I antigen heavy chain precursor.  
 GN HLA-B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96128250; PubMed=85371119;

RA Smith K.D., Epperson D.F., Lutz C.T.;  
 RT "Alloreactive cytotoxic T-lymphocyte-defined HLA-B7 subtypes differ in  
 RT peptide antigen presentation.";  
 RL Immunogenetics 43:27-37(1996).  
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE  
 CC IMMUNE SYSTEM (BY SIMILARITY).  
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-  
 CC MICROGLOBULIN) (BY SIMILARITY).  
 DR EMBL; U21053; AAA92564.1; -.  
 DR HSSP; P30460; IJAG.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PRO1638; MHCCLASSI.  
 DR PRODOM; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; Igcl; 1.  
 DR PROSITE; PS00290; Ig\_MHC; 1.  
 KW Glycoprotein; Signal; Transmembrane.  
 FT SIGNAL 1 24  
 FT CHAIN 25 362 MHC CLASS I ANTIGEN HEAVY CHAIN.  
 SQ SEQUENCE 362 AA; 40506 MW; 563D142F5507BC98 CRC64;

Query Match 34.8%; Score 523; DB 7; Length 362;  
 Best local similarity 39.6%; Pred. No. 4.3e-37;  
 Matches 112; Conservative 49; Mismatches 112; Indels 10; Gaps 7;

QY 2 ENODGRSLTYITVGLSKHVEDPAPFQALGSLNDLOEFRRYS--KDRKSQPMGLMROVEG 59  
 Db 21 ETWAGSHSMRYFTYSVRSGRGPREFISGVYDDTQFVRFSDDAASPREBRRAWIEDEG 80  
 QY 60 MEDKEDSOLOK--AREMETLKDIIVEYNDN--GSHVLQGRFGEI--ENNRSSGAFWKY 115  
 Db 81 PEYMDRNTQITKTNTQDRESLRNLRGYNDSEAGSHTLQSMYGGDMDPDRLLRGHDY 140  
 QY 116 YDDKDYIEFKETIPAWPFPDPAOITKQKWEAEPPVYVQRAKAYLEECPTLTKRYLYKS 175  
 Db 141 AYDGDYIALNWDLSRWADTAOITQKWEARENR--RAYLEGCVEMLRYLENG 199  
 QY 176 KNILRDPPPSVVVTSHQAPGEKKLKCLAYDFYPGKIDVHWTRAG--QVOEPELRGDVL 233  
 Db 200 KDKLERADPRKTHVTHHPSIDEHATLRQWALGFYPAETITLWQDGEEDQTDTEL-VETR 258  
 QY 234 HNGKTYOSWVVAVPPDPTAPYCHVQHSSLAQPLVVPWEAS 276  
 Db 259 PAGDRTFQKMAVVVPSGEQRYTCHVQHEGLPKPLTLRWEPS 301  
 RESULT 10  
 Q9MKK4 PRELIMINARY; PRT; 362 AA.  
 ID Q9MKK4;  
 AC Q9MKK4;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE MHC class I antigen (lymphocyte antigen).  
 GN PATR-B OR PATR-B17.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
 RX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=20322475; PubMed=10866106;  
 RA de Groot N.G., Olling N., Arguello R., Watkins D.I., Doxiadis G.G.,  
 RA Madrigal J.A., Bontrop R.E.;  
 RT "Major histocompatibility complex class I diversity in a West African  
 chimpanzee population: implications for HIV research.";  
 RL Immunogenetics 51:398-409(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.





```

Db 13 ETWASHSHSRKYTSVSRGRGEPRFTYGVYDDTQFVAFEDDAASPRMEPRAPWIEQEG 72
QY 60 MEDMKEDSOLOK--AREDETLDIVYEYNDSDN-GSHVLQGRFGEI-ENNSSSAFWMY 115
Db 73 PEYWDRETRNMKASQOTDRENLRIALRYNOSSEASHIIOGRYGGDMGDLGLNGYQY 132
QY 116 YYDGKDYIEFNKEIPAWVPDPAAQITQKWEAEPPYVORAKAYLEECBPATLRKYLKYS 175
Db 133 AYDGKDYIALNEDLSSWTAADTAQAQITQKWEAARAQR-RAYLEGTCEVWLRRLYLENG 191
QY 176 KNIIDRDPSPVYVTSQAPEKKKLCIAYFPYFKIDVHTFRAG--QVQPELRGDVL 233
Db 192 KETLGRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTDTEL-VETR 250
QY 234 HNGNGTQSWVYVAVPPODTAPYSCHVQSSLAQPLVYVMEAS 276
Db 251 PEGDRTFQKMAVAVVPSGGEQRYTCHVQHEGLPKPPLTLRMEPS 293

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## RESULT 15

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ID 095529 PRELIMINARY: PRT: 355 AA.
AC 095529:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
ET 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
FF 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Class I histocompatibility antigen (Fragment).
GN HLA-B.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_Taxid=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TEPRF.
RX MEDLINE=9428654; PubMed=8016085;
RA McAdam S.N., Boyson J.E., Liu X., Garber T.L., Hughes A.L.,
RA Bontrop R.E., Watkins D.I.;
RT "A uniquely high level of recombination at the HLA-B locus.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC -I- IMMUNE SYSTEM (BY SIMILARITY).
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
CC EMBL: U05580; AAA50183.1; -.
DR HSSP: P03989; IHS.
DR InterPro: IPR003597; Ig_CL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR01039; MHC_I.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00129; MHC_I; 1.
DR PRINTS: PR01638; MHCCLASSI.
DR PRODOM: PD000050; MHC_I; 1.
DR SMART: SM00407; IgCL; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Glycoprotein; Transmembrane.
FT NON_TER
SQ SEQUENCE 355 AA: 39772 MW: F474A2C3EEDC398A CRC64:

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Query Match 34.6%; Score 521; DB 7; Length 355;  
 Best Local Similarity 38.9%; Pred. No. 6.2e-37;  
 Matches 110; Conservative 48; Mismatches 115; Indels 10; Gaps 7;

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QY 2 ENDGGRYSLTYYITGLSKHVEDPAPQALGSLNDLOFFRYS--KDRKSQPMGLMROVGS 59
Db 13 ETWAGSHSMKYFTSVSRGRGEPRFTYGVYDDTQFVAFEDDAASPRMEPRAPWIEQEG 72
QY 60 MEDMKEDSOLOK--AREDETLDIVYEYNDSDN-GSHVLQGRFGEI-ENNSSSAFWMY 115
Db 73 PEYWDRETRNMKASQOTDRENLRIALRYNOSSEASHIIOGRYGGDMGDLGLNGYQY 132
QY 116 YYDGKDYIEFNKEIPAWVPDPAAQITQKWEAEPPYVORAKAYLEECBPATLRKYLKYS 175

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Db 133 AYDGKDYIALNEDLSSWTAADTAQAQITQKWEAARAQR-RAYLEGTCEVWLRRLYLENG 191
QY 176 KNIIDRDPSPVYVTSQAPEKKKLCIAYFPYFKIDVHTFRAG--QVQPELRGDVL 233
Db 192 KETLGRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTDTEL-VETR 250
QY 234 HNGNGTQSWVYVAVPPODTAPYSCHVQSSLAQPLVYVMEAS 276
Db 251 PEGDRTFQKMAVAVVPSGGEQRYTCHVQHEGLPKPPLTLRMEPS 293

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 Job time : 35 secs